



# STIC Search Report

## Biotech-Chem Library

STIC Database Tracking Number: 159142

TO: Ruixiang Li  
Location: rem/4D75/4C70  
Art Unit: 1646  
Friday, July 15, 2005

Case Serial Number: 10/019151

From: Edward Hart  
Location: Biotech-Chem Library  
REM-1A55  
Phone: 571-272-2512

[edward.hart@uspto.gov](mailto:edward.hart@uspto.gov)

### Search Notes

Examiner Li,

Here are the results of the search you requested.

Please feel free to contact me if you have any questions.

Edward Hart

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## STIC-Biotech/ChemLib

159142

mg

From: Li, Ruixiang  
Sent: Tuesday, July 12, 2005 7:09 PM  
To: STIC-Biotech/ChemLib  
Subject: Sequence search of Application No.10/019,151

Please do a standard search on:

SEQ ID NOS: 1-3 against commercial amino acid databases.

Thank you very much!

Ruixiang Li  
GAU 1646  
REM 4D75  
Mail Box 4C70  
(571) 272-0875

STIC  
JUL 13 2005  
15:10

\*\*\*\*\*

## STAFF USE ONLY

Searcher: \_\_\_\_\_  
Searcher Phone: 2- \_\_\_\_\_  
Date Searcher Picked up: 7/15/05  
Date Completed: 7/15/05  
Searcher Prep/Rev. Time: \_\_\_\_\_  
Online Time: \_\_\_\_\_

\*\*\*\*\*

## Type of Search

NA#: \_\_\_\_\_ AA#: 3  
Interference: \_\_\_\_\_ SPDI: \_\_\_\_\_  
S/L: \_\_\_\_\_ Oligomer: \_\_\_\_\_  
Encode/Transl: \_\_\_\_\_  
Structure#: \_\_\_\_\_ Text: \_\_\_\_\_  
Inventor: \_\_\_\_\_ Litigation: \_\_\_\_\_

\*\*\*\*\*

## Vendors and cost where applicable

STN: \_\_\_\_\_  
DIALOG: \_\_\_\_\_  
QUESTEL/ORBIT: \_\_\_\_\_  
LEXIS/NEXIS: \_\_\_\_\_  
SEQUENCE SYSTEM: QSP  
WWW/Internet: \_\_\_\_\_  
Other(Specify): \_\_\_\_\_

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CC sequences. The invention provides polynucleotides (see AAY57946-55) from  
 CC foetal brain, adult testis, adult brain, adult kidney and foetal kidney  
 CC (all deposited as ATCC 98404), which encode human secreted proteins (see  
 CC AAY4720-29). The polynucleotides and proteins are predicted to have  
 CC biological activities which would make them suitable for treating,  
 CC preventing or ameliorating medical conditions in humans and animals.  
 CC although no supporting data are given. Suggested activities include  
 CC nutritional, immune stimulating (e.g. as vaccines) or suppressing  
 CC activity, haematopoiesis regulating activity, tissue growth activity,  
 CC activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic  
 CC and thrombolytic activity, receptor/ligand activity, anti-inflammatory  
 CC activity, cadherin/tumour invasion suppressor activity, and tumour  
 CC inhibition activity

XX Sequence 339 AA;

Query Match 100.0%; Score 1879; DB 2; Length 339;  
 Best Local Similarity 100.0%; Pred. No. 8.6e-162;  
 Matches 339; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAACGPGAGYCLLGLHFLTLTAPALGNDPRLMLRDYKALTLHYDRYTSRLDP 60  
 DB 1 MAACGPGAGYCLLGLHFLTLTAPALGNDPRLMLRDYKALTLHYDRYTSRLDP 60  
 QY 61 IPOLKCVGTAGCDSTPKVIOCKNGMDGVQVQECTDLDIAKFGKTVVSCGYESS 120  
 DB 61 IPOLKCVGTAGCDSTPKVIOCKNGMDGVQVQECTDLDIAKFGKTVVSCGYESS 120  
 QY 121 EDQVLRSGCGLENYLDYTELGLOKLSGKOHGPAFSFYKMSADSCKMSGLITIV 180  
 DB 121 EDQVLRSGCGLENYLDYTELGLOKLSGKOHGPAFSFYKMSADSCKMSGLITIV 180  
 QY 181 VLLGIAFVYVKLFLSDQVSPPPYSEYPPSHRYQRTNSAGPPPGFKSEFTGPONTGH 240  
 DB 181 VLLGIAFVYVKLFLSDQVSPPPYSEYPPSHRYQRTNSAGPPPGFKSEFTGPONTGH 240  
 QY 241 GATSGFGSAFTGQGGYENSGPGFWTGLGTGILGTLFGSNRAATPPSDSYTPSPSYP 300  
 DB 241 GATSGFGSAFTGQGGYENSGPGFWTGLGTGILGTLFGSNRAATPPSDSYTPSPSYP 300  
 QY 301 GTMNRAYSPLHSGSGSYVCSNDDTKRTTASGYGTRRR 339  
 DB 301 GTMNRAYSPLHSGSGSYVCSNDDTKRTTASGYGTRRR 339

RESULT 2  
 AAY57943  
 ID AAY57943 standard; protein; 339 AA.

XX AAY57943;

XX 23-MAR-2000 (first entry)

XX Human transmembrane protein HTMPN-67.

XX Human transmembrane protein; HTMPN; diagnosis; immunospecific;  
 KW anti-proliferative; neuroprotective; immune disorder;  
 KW reproductive disorder; smooth muscle disorder; neurological disorder;  
 KW gastrointestinal disorder; developmental disorder;  
 KW cell proliferative disorder.

XX Homo sapiens.

XX MO9961471-A2.

XX 02-DEC-1999.

XX 28-MAY-1999; 99MO-US011904.

XX 29-MAY-1998; 98US-0087260P.

XX 02-JUL-1998; 98US-0891674P.

XX 02-OCT-1998; 98US-0108954P.

XX 24-NOV-1998; 98US-0108463P.

XX (INCY-) INCYTE PHARM INC.

XX Tang YT, Lal P, Hillman JL, Yue H, Guegler KJ, Corley NC;  
 PI Bandman O, Patterson C, Gorgone GA, Kaeser MR, Baughn MR, Au-Young J;  
 DR WPI; 2000-072605/06.

DR N-PSDB; AAY56764.

XX proteins, polynucleotides, vectors, host cells and antibodies used to  
 XX diagnose, treat or prevent immune, reproductive, smooth muscle,  
 XX neurological, gastrointestinal, developmental and cell proliferative  
 XX disorders.

XX Claim 1; Page 166-167; 229pp; English.

XX AAY56798 to AAY56776 encode AAY57877 to AAY57955 which represent human  
 CC transmembrane proteins designated HTMPN-1 to HTMPN-79, respectively. The  
 CC transmembrane protein have immunospecific, antiproliferative and  
 CC neuroprotective activities. The human transmembrane proteins,  
 CC polynucleotides encoding them and other compositions and methods from the  
 CC present invention, can be used for the diagnosis, treatment or prevention  
 CC of immune, reproductive, smooth muscle, neurological, gastrointestinal,  
 CC developmental and cell proliferative disorders. The HTMPN's can be used  
 CC to treat or prevent disorders associated with a decreased expression or  
 CC activity of HTMPN

XX Sequence 339 AA;

Query Match 100.0%; Score 1879; DB 3; Length 339;  
 Best Local Similarity 100.0%; Pred. No. 8.6e-162;  
 Matches 339; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAACGPGAGYCLLGLHFLTLTAPALGNDPRLMLRDYKALTLHYDRYTSRLDP 60  
 DB 1 MAACGPGAGYCLLGLHFLTLTAPALGNDPRLMLRDYKALTLHYDRYTSRLDP 60  
 QY 61 IPOLKCVGTAGCDSTPKVIOCKNGMDGVQVQECTDLDIAKFGKTVVSCGYESS 120  
 DB 61 IPOLKCVGTAGCDSTPKVIOCKNGMDGVQVQECTDLDIAKFGKTVVSCGYESS 120  
 QY 121 EDQVLRSGCGLENYLDYTELGLOKLSGKOHGPAFSFYKMSADSCKMSGLITIV 180  
 DB 121 EDQVLRSGCGLENYLDYTELGLOKLSGKOHGPAFSFYKMSADSCKMSGLITIV 180  
 QY 181 VLLGIAFVYVKLFLSDQVSPPPYSEYPPSHRYQRTNSAGPPPGFKSEFTGPONTGH 240  
 DB 181 VLLGIAFVYVKLFLSDQVSPPPYSEYPPSHRYQRTNSAGPPPGFKSEFTGPONTGH 240  
 QY 241 GATSGFGSAFTGQGGYENSGPGFWTGLGTGILGTLFGSNRAATPPSDSYTPSPSYP 300  
 DB 241 GATSGFGSAFTGQGGYENSGPGFWTGLGTGILGTLFGSNRAATPPSDSYTPSPSYP 300  
 QY 301 GTMNRAYSPLHSGSGSYVCSNDDTKRTTASGYGTRRR 339  
 DB 301 GTMNRAYSPLHSGSGSYVCSNDDTKRTTASGYGTRRR 339

RESULT 3

XX AAY70117  
 ID AAY70117 standard; protein; 339 AA.

XX AAY70117;

XX 06-JUN-2000 (first entry)

XX Human ischaemic heart disease associated protein, PGP980.1.

XX ischaemia; heart disease; human; PGP980.1; cardiomyopathy; cardiac;  
 KW modulator; treat; prevention; diagnosis.

XX Homo sapiens.

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CC sequences. The invention provides polynucleotides (see AAV62746-55) from  
 CC foetal brain, adult testis, adult brain, adult kidney and foetal kidney  
 CC (all deposited as ATCC 98404), which encode human secreted proteins (see  
 CC AAV74720-29). The polynucleotides and proteins are predicted to have  
 CC biological activities which would make them suitable for treating,  
 CC preventing or ameliorating medical conditions in humans and animals,  
 CC although no supporting data are given. Suggested activities include  
 CC nutritional, immune stimulating (e.g. as vaccine) or suppressing  
 CC activity, haematopoiesis regulating activity, tissue growth activity,  
 CC actinin/inhibin activity, chemocytic/chemokinetic activity, haemostatic  
 CC and thrombolytic activity, chemokine/ligand activity, anti-inflammatory  
 CC activity, cadherin/tumour invasion suppressor activity, and tumour  
 CC inhibition activity

XX Sequence 339 AA;

Query Match 100.0%; Score 1879; DB 2; Length 339;  
 Best Local Similarity 100.0%; Pred. No. 8.6e-162;  
 Matches 339; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAACGPGAGYCLLGLHLFLITAGPALGMDPDRMLRDYKALTLHYDRYTSRRLLDP 60  
 DB 1 MAACGPGAGYCLLGLHLFLITAGPALGMDPDRMLRDYKALTLHYDRYTSRRLLDP 60  
 QY 61 IPOLKCVGTAGGDSYTPKVIQCONKGMGDYDVQMECKTDLDIAVYKFGTVSCGEYSS 120  
 DB 61 IPOLKCVGTAGGDSYTPKVIQCONKGMGDYDVQMECKTDLDIAVYKFGTVSCGEYSS 120  
 QY 121 EDQYVLRGSCGLEYNLDYTELGLOKLKESGKHGFASPSDYKKMSADSCKMSGLITIV 180  
 DB 121 EDQYVLRGSCGLEYNLDYTELGLOKLKESGKHGFASPSDYKKMSADSCKMSGLITIV 180  
 QY 181 VLLGIAFVYVKLFLSDGQYSPPEYSEYPPFSHRVQFTNSAGPPPGFSEFTGPONTGH 240  
 DB 181 VLLGIAFVYVKLFLSDGQYSPPEYSEYPPFSHRVQFTNSAGPPPGFSEFTGPONTGH 240  
 QY 241 GATSGFGSAFTGQOQYENSGPGFWTGLGTGILGYLFGSNRAATPPSDSWYPSYPSYP 300  
 DB 241 GATSGFGSAFTGQOQYENSGPGFWTGLGTGILGYLFGSNRAATPPSDSWYPSYPSYP 300  
 QY 301 GTWNRAYSPLHGGSGSYVCSNSDTKRTTASGYGTRRR 339  
 DB 301 GTWNRAYSPLHGGSGSYVCSNSDTKRTTASGYGTRRR 339

RESULT 2  
 AAY57943  
 ID AAY57943 standard; protein; 339 AA.

XX AAY57943;  
 AC AAY57943;  
 XX  
 DT 23-MAR-2000 (first entry)  
 XX  
 DE Human transmembrane protein HTMPN-67.  
 XX  
 KW Human: transmembrane protein; HTMPN, diagnosis; immunospecific;  
 KW antiproliferative; neuroprotective; immune disorder;  
 KW reproductive disorder; smooth muscle disorder; neurological disorder;  
 KW gastrointestinal disorder; developmental disorder;  
 KW cell proliferative disorder.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO9961471-A2.  
 XX  
 PD 02-DEC-1999.  
 XX  
 PF 28-MAY-1999; 99WO-US011904.  
 XX  
 PR 29-MAY-1998; 98US-0087260P.  
 \*PR 02-JUL-1998; 98US-0091674P.  
 PR 02-OCT-1998; 98US-0102954P.  
 PR 24-NOV-1998; 98US-0109869P.

XX (INCY-) INCYTE PHARM INC.

PA Tang YT, Lal P, Hillman JL, Yue H, Guegler KJ, Corley NC;  
 PI Bandman O, Patterson C, Gorgone GA, Kaser MR, Baughn MR, Au-Young J;  
 DR WPI; 2000-072605/06.  
 N-PSDB; AA256764.

XX Proteins, polynucleotides, vectors, host cells and antibodies used to  
 PT diagnose, treat or prevent immune, reproductive, smooth muscle,  
 PT neurological, gastrointestinal, developmental and cell proliferative  
 PT disorders.

XX Claim 1; Page 166-167; 229pp; English.

CC AA256698 to AA256776 encode AAY57877 to AAY57955 which represent human  
 CC transmembrane proteins designated HTMPN-1 to HTMPN-79, respectively. The  
 CC transmembrane protein have immunospecific, antiproliferative and  
 CC neuroprotective activities. The human transmembrane proteins,  
 CC polynucleotides encoding them and other compositions and methods from the  
 CC present invention, can be used for the diagnosis, treatment or prevention  
 CC of immune, reproductive, smooth muscle, neurological, gastrointestinal,  
 CC developmental and cell proliferative disorders. The HTMPN's can be used  
 CC to treat or prevent disorders associated with a decreased expression or  
 CC activity of HTMPN

XX Sequence 339 AA;

Query Match 100.0%; Score 1879; DB 3; Length 339;  
 Best Local Similarity 100.0%; Pred. No. 8.6e-162;  
 Matches 339; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAACGPGAGYCLLGLHLFLITAGPALGMDPDRMLRDYKALTLHYDRYTSRRLLDP 60  
 DB 1 MAACGPGAGYCLLGLHLFLITAGPALGMDPDRMLRDYKALTLHYDRYTSRRLLDP 60  
 QY 61 IPOLKCVGTAGGDSYTPKVIQCONKGMGDYDVQMECKTDLDIAVYKFGTVSCGEYSS 120  
 DB 61 IPOLKCVGTAGGDSYTPKVIQCONKGMGDYDVQMECKTDLDIAVYKFGTVSCGEYSS 120  
 QY 121 EDQYVLRGSCGLEYNLDYTELGLOKLKESGKHGFASPSDYKKMSADSCKMSGLITIV 180  
 DB 121 EDQYVLRGSCGLEYNLDYTELGLOKLKESGKHGFASPSDYKKMSADSCKMSGLITIV 180  
 QY 181 VLLGIAFVYVKLFLSDGQYSPPEYSEYPPFSHRVQFTNSAGPPPGFSEFTGPONTGH 240  
 DB 181 VLLGIAFVYVKLFLSDGQYSPPEYSEYPPFSHRVQFTNSAGPPPGFSEFTGPONTGH 240  
 QY 241 GATSGFGSAFTGQOQYENSGPGFWTGLGTGILGYLFGSNRAATPPSDSWYPSYPSYP 300  
 DB 241 GATSGFGSAFTGQOQYENSGPGFWTGLGTGILGYLFGSNRAATPPSDSWYPSYPSYP 300  
 QY 301 GTWNRAYSPLHGGSGSYVCSNSDTKRTTASGYGTRRR 339  
 DB 301 GTWNRAYSPLHGGSGSYVCSNSDTKRTTASGYGTRRR 339

RESULT 3  
 AAY70117  
 ID AAY70117 standard; protein; 339 AA.

XX AAY70117;  
 AC AAY70117;  
 XX  
 DT 06-JUN-2000 (first entry)  
 XX  
 DE Human ischaemic heart disease associated protein, GGP980.1.  
 XX  
 KW Ischaemia; heart disease; human; GGP980.1; cardiomyopathy; cardiac;  
 KW modulator; treat; prevention; diagnosis.  
 XX  
 OS Homo sapiens.

Key Location/Qualifiers  
Peptide 1..29  
Protein 30..339  
/label= Mature\_human\_PGP980.1 protein  
/note= "Ischaemic heart disease associated protein"

XX MO200011942-A1.  
XX 09-MAR-2000.  
XX 01-SEP-1999; 99WC-US020015.  
XX 01-SEP-1998; 98US-0098683P.  
XX (GENE-) GENE LOGIC INC.  
XX Elmslein R;  
XX WPI; 2000-237720/20.  
XX N-PSDB; AAZ51193.  
XX Isolated nucleic acids encoding a proteins that is differentially  
XX expressed during ischemic heart disease and ischemic cardiomyopathy,  
XX useful for preventing, diagnosing and treating cardiac disease.  
XX Claim 14; Page 50-51; 61pp; English.  
XX The present amino acid sequence is the human protein designated as  
XX PGP980.1, that is differentially expressed in ischaemic heart disorders.  
XX PGP980.1 is isolated from human heart cDNA library and is expressed in  
XX heart, brain, placenta, lung, skeletal muscle, kidney and pancreas. This  
XX sequence is homologous to PGP980.2 protein, but differs at position 66,  
XX wherein PGP980.2 has arginine residue. PGP980.1 has cardiant activity.  
XX The DNA may be used as probes to detect and quantify homologous sequences  
XX in samples. PGP980.1 sequences can be used to identify modulators, that  
XX can be used for treatment, diagnosis and prevention of diseases  
XX associated with inappropriate expression and activity of the protein,  
XX such as ischaemic heart disease and ischaemic cardiomyopathy  
XX Sequence 339 AA;  
XX

Query Match 100.0%; Score 1879; DB 3; Length 339;  
Best Local Similarity 100.0%; Pred. No. 8.6e-162;  
Matches 339; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAAACGPGAGYCLLGLHLFLITAGPALGMDPDRMLADVATLTLYDRYTSRRLD 60  
DB 1 MAAACGPGAGYCLLGLHLFLITAGPALGMDPDRMLADVATLTLYDRYTSRRLD 60  
QY 61 IYOLKVGSTAGCDSTTPKVIQCONKGMQDYDVQWCKTDLDIAYKRGKTVSCGEYSS 120  
DB 61 IYOLKVGSTAGCDSTTPKVIQCONKGMQDYDVQWCKTDLDIAYKRGKTVSCGEYSS 120  
QY 121 EDQYVLRGSCGLEYNIDYTELGQKLKESGKHGPFSPDYKYKMSADSCKNSGLITTY 180  
DB 121 EDQYVLRGSCGLEYNIDYTELGQKLKESGKHGPFSPDYKYKMSADSCKNSGLITTY 180  
QY 181 VLLGLAFVYVKLFLSDQYSPPPYSEYPPESHRYQRTNSAGPPGPFKSEFTGPNTH 240  
DB 181 VLLGLAFVYVKLFLSDQYSPPPYSEYPPESHRYQRTNSAGPPGPFKSEFTGPNTH 240  
QY 241 GATSGGSAFTGQGGYENSGRGWTLGTGGLIGYLPGRATTPSDSYTYSPSP 300  
DB 241 GATSGGSAFTGQGGYENSGRGWTLGTGGLIGYLPGRATTPSDSYTYSPSP 300  
QY 301 GTWNRAYSPLHGSGSYVCSNSDTKTRTASGYGTRRR 339  
DB 301 GTWNRAYSPLHGSGSYVCSNSDTKTRTASGYGTRRR 339

ID AAB18931 standard; protein; 339 AA.  
XX AAB18931;  
AC 08-FEB-2001 (first entry)  
XX A novel polypeptide designated PRO4499.  
XX  
XX Secreted protein; transmembrane protein; PRO1484; PRO4334; PRO1122;  
XX PRO1889; PRO1880; PRO1887; PRO1785; PRO4353; PRO4357; PRO4356;  
XX PRO4352; PRO4380; PRO4354; PRO4408; PRO5737; PRO4425; PRO5990; PRO6030;  
XX PRO4424; PRO4423; PRO4422; tumour; obesity; diabetes;  
XX insulinemia; kidney disorder; Bergers disease; nephropathy;  
XX Schomlein-Henoch purpura; celliac disease; dermatitis herpetiformis;  
XX Crohns disease.  
XX Homo sapiens.  
XX  
XX Key Location/Qualifiers  
XX Peptide 1..30  
XX /note= "signal sequence"  
XX Modified-site 68..74  
XX /note= "N-myristoylation site"  
XX Modified-site 69..75  
XX /note= "N-myristoylation site"  
XX Modified-site 98..106  
XX /note= "tyrosine kinase phosphorylation site"  
XX Modified-site 131..137  
XX /note= "N-myristoylation site"  
XX Domain 171..190  
XX /note= "transmembrane domain"  
XX Modified-site 172..176  
XX /note= "N-glycosylation site"  
XX Modified-site 241..247  
XX /note= "N-myristoylation site"  
XX Modified-site 247..253  
XX /note= "N-myristoylation site"  
XX Modified-site 266..272  
XX /note= "N-myristoylation site"  
XX Modified-site 270..276  
XX /note= "N-myristoylation site"  
XX Modified-site 278..284  
XX /note= "N-myristoylation site"  
XX Modified-site 312..318  
XX /note= "N-myristoylation site"  
XX  
XX MO200056889-A2.  
XX 28-SEP-2000.  
XX  
XX 01-MAR-2000; 2000WC-US005601.  
XX 23-MAR-1999; 99US-0125774P.  
XX 23-MAR-1999; 99US-0125778P.  
XX 24-MAR-1999; 99US-0125826P.  
XX 31-MAR-1999; 99US-0127035P.  
XX 05-APR-1999; 99US-0127706P.  
XX 21-APR-1999; 99US-0130359P.  
XX 21-APR-1999; 99US-0131270P.  
XX 27-APR-1999; 99US-0131272P.  
XX 27-APR-1999; 99US-0131291P.  
XX 04-MAY-1999; 99US-0132371P.  
XX 04-MAY-1999; 99US-0132379P.  
XX 04-MAY-1999; 99US-0132383P.  
XX 25-MAY-1999; 99US-0135750P.  
XX 08-JUN-1999; 99US-0138166P.  
XX 20-JUL-1999; 99US-0144791P.  
XX 03-AUG-1999; 99US-0146970P.  
XX 09-DEC-1999; 99US-0170262P.  
XX  
XX (GENE ) GENENTECH INC.  
XX Desnoyers L, Bacon DL, Goddard A, Godowski PJ, Gurney AL, Pan J,

PI Stewart TA, Watanabe CK, Wood WI, Zhang Z;  
 XX WPI, 2000-628263/60.  
 DR N-PSDB; AAA96358.  
 XX  
 PT Novel secreted and transmembrane polypeptides useful for diagnosing tumor  
 PT in a mammal, for identifying agonists and antagonists of the polypeptide  
 PT and for therapeutic use.  
 XX  
 PS Claim 12, Fig 46; 222pp; English.  
 XX  
 CC The present sequence represents a secreted or transmembrane polypeptide.  
 CC The specification describes polypeptides designated PRO1484, PRO4334,  
 CC PRO1322, PRO1889, PRO1890, PRO1887, PRO1785, PRO4353, PRO4357, PRO4405,  
 CC PRO4356, PRO4352, PRO4380, PRO4354, PRO4408, PRO5737, PRO4425, PRO5990,  
 CC PRO6030, PRO4434, PRO4430, PRO4432, PRO4430 and PRO4499. PRO1889 polypeptide is  
 CC useful for diagnosing tumor in a mammal. The polypeptides, their  
 CC agonists and antagonists are useful treating a condition associated with  
 CC expression or activity of the polypeptide. Conditions treated include  
 CC obesity, diabetes or hyper- or hypo-insulinemia. The polypeptides are  
 CC capable of inducing proliferation of mammalian kidney mesangial cells and  
 CC are therefore useful for treating kidney disorders associated with  
 CC decreased mesangial cell function such as Berger's disease or other  
 CC nephropathies associated with Schönlein-Henoch purpura, celiac disease,  
 CC dermatitis herpetiformis or Crohn's disease. The nucleic acids may be used  
 CC to generate transgenic animals for use in development and screening of  
 CC therapeutically useful reagents and also for chromosome identification  
 CC and tissue typing  
 CC  
 XX  
 XX Sequence 339 AA;  
 SQ  
 Query Match 100.0%; Score 1879; DB 3; Length 339;  
 Best Local Similarity 100.0%; Pred. No. 8.6e-162;  
 Matches 339; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MAAACGPGAAAGCYLLGLHLFLTTAGPALGMPDPRMLRDVKALTLHYDRYTSRRLLP 60  
 DB 1 MAAACGPGAAAGCYLLGLHLFLTTAGPALGMPDPRMLRDVKALTLHYDRYTSRRLLP 60  
 QY 61 IPOLKCVGTAGCDSTTPKVIQCONKGMGVDYVQMECKTDLDIAVYFKTIVSCGEYESS 120  
 DB 61 IPOLKCVGTAGCDSTTPKVIQCONKGMGVDYVQMECKTDLDIAVYFKTIVSCGEYESS 120  
 QY 121 EDGYVLRGSCGLEYNLDYTELGLOKLKESGKHGFASFSYIYKMSADSCKMSGLITTV 180  
 DB 121 EDGYVLRGSCGLEYNLDYTELGLOKLKESGKHGFASFSYIYKMSADSCKMSGLITTV 180  
 QY 121 EDGYVLRGSCGLEYNLDYTELGLOKLKESGKHGFASFSYIYKMSADSCKMSGLITTV 180  
 DB 121 EDGYVLRGSCGLEYNLDYTELGLOKLKESGKHGFASFSYIYKMSADSCKMSGLITTV 180  
 QY 181 VLLGIAFVYVYKFLPSDGOYSPPPYSEYPPFSHRVQRFNLSAGPPPGFSEFTGQNTGH 240  
 DB 181 VLLGIAFVYVYKFLPSDGOYSPPPYSEYPPFSHRVQRFNLSAGPPPGFSEFTGQNTGH 240  
 QY 241 GATSGFGSAFTGQOQYENSGPGFMTGLGTGILGYLFGSNRAATPFSDSWYTPSPSP 300  
 DB 241 GATSGFGSAFTGQOQYENSGPGFMTGLGTGILGYLFGSNRAATPFSDSWYTPSPSP 300  
 QY 301 GTMNRAVSPPLHGGSGSYVCSNSDTRKTRTASGYGTRRR 339  
 DB 301 GTMNRAVSPPLHGGSGSYVCSNSDTRKTRTASGYGTRRR 339  
 RESULT 5  
 AAB19395  
 ID AAB19395 standard; protein; 339 AA.  
 XX  
 AC AAB19395;  
 XX  
 DT 06-MAR-2001 (first entry)  
 XX  
 DE Amino acid sequence of a human secreted protein.  
 XX  
 XX Secreted protein; platelet disorder; stem cell disorder; osteoporosis;  
 KM osteoarthritis; burn; incision; ulcer; periodontal disease; neuropathy;  
 KM nervous system disease; bone growth; cosmetic plastic surgery;

KM gut protection; gut regeneration; fibrosis; cancer;  
 KM bone marrow transplantation.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200061755-A2.  
 XX  
 PD 19-OCT-2000.  
 XX  
 PF 10-APR-2000; 2000MO-US009555.  
 XX  
 PR 09-APR-1999; 99US-0128574P.  
 PR 20-AUG-1999; 99US-0150054P.  
 XX  
 PA (CHIR ) CHIRON CORP.  
 XX  
 PI Garcia PD;  
 XX  
 DR WPI; 2000-665133/64.  
 DR N-PSDB; AAC61881.  
 XX  
 PT Novel secreted human proteins useful for stimulating blood cell  
 PT generation in patients receiving cancer chemotherapy, treating bone  
 PT marrow transplantation patients and for healing fractured bones.  
 XX  
 PS Claim 14; Page 56; 74pp; English.  
 XX  
 CC AAB19395-B19407 represent secreted human proteins. The secreted proteins  
 CC are useful in assays to determine their biological activities. The  
 CC proteins can also be used as biomarkers to identify tissues or cell types  
 CC which express the proteins. The polynucleotide molecules can be used as  
 CC biomarkers for tissues or chromosomes and to elicit immune responses. The  
 CC proteins and antibodies are useful in diagnosis and treatment of diseases  
 CC associated with altered expression of these proteins. The proteins are  
 CC also useful for prevention or treatment of platelet disorders, stem cell  
 CC disorders, osteoporosis or osteoarthritis, burns, incisions, ulcers,  
 CC periodontal diseases, central and peripheral nervous system diseases and  
 CC neuropathies, for healing fractured bones and to induce cartilage and/or  
 CC bone growth in cosmetic plastic surgery. The proteins are also useful for  
 CC gut protection or regeneration, for the treatment of lung or liver  
 CC fibrosis, for stimulating blood cell generation in patients receiving  
 CC cancer chemotherapy and for treatment of bone marrow transplantation  
 CC patients  
 CC  
 XX  
 XX Sequence 339 AA;  
 SQ  
 Query Match 100.0%; Score 1879; DB 3; Length 339;  
 Best Local Similarity 100.0%; Pred. No. 8.6e-162;  
 Matches 339; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MAAACGPGAAAGCYLLGLHLFLTTAGPALGMPDPRMLRDVKALTLHYDRYTSRRLLP 60  
 DB 1 MAAACGPGAAAGCYLLGLHLFLTTAGPALGMPDPRMLRDVKALTLHYDRYTSRRLLP 60  
 QY 61 IPOLKCVGTAGCDSTTPKVIQCONKGMGVDYVQMECKTDLDIAVYFKTIVSCGEYESS 120  
 DB 61 IPOLKCVGTAGCDSTTPKVIQCONKGMGVDYVQMECKTDLDIAVYFKTIVSCGEYESS 120  
 QY 121 EDGYVLRGSCGLEYNLDYTELGLOKLKESGKHGFASFSYIYKMSADSCKMSGLITTV 180  
 DB 121 EDGYVLRGSCGLEYNLDYTELGLOKLKESGKHGFASFSYIYKMSADSCKMSGLITTV 180  
 QY 121 EDGYVLRGSCGLEYNLDYTELGLOKLKESGKHGFASFSYIYKMSADSCKMSGLITTV 180  
 DB 121 EDGYVLRGSCGLEYNLDYTELGLOKLKESGKHGFASFSYIYKMSADSCKMSGLITTV 180  
 QY 181 VLLGIAFVYVYKFLPSDGOYSPPPYSEYPPFSHRVQRFNLSAGPPPGFSEFTGQNTGH 240  
 DB 181 VLLGIAFVYVYKFLPSDGOYSPPPYSEYPPFSHRVQRFNLSAGPPPGFSEFTGQNTGH 240  
 QY 241 GATSGFGSAFTGQOQYENSGPGFMTGLGTGILGYLFGSNRAATPFSDSWYTPSPSP 300  
 DB 241 GATSGFGSAFTGQOQYENSGPGFMTGLGTGILGYLFGSNRAATPFSDSWYTPSPSP 300  
 QY 301 GTMNRAVSPPLHGGSGSYVCSNSDTRKTRTASGYGTRRR 339  
 DB 301 GTMNRAVSPPLHGGSGSYVCSNSDTRKTRTASGYGTRRR 339



## RESULT 6

AAB20090  
ID AAB20090 standard; protein; 339 AA.

AC AAB20090;

DT 23-APR-2001 (first entry)

DE Human hydrophobic domain-containing protein HP03342.

XX Human; hydrophobic domain; antiinflammatory; immunosuppressive;  
XX immunostimulant; vulnerracy; antitumor; haemostatic; cytostatic;  
XX hepatocytic; thrombolytic; antitumor; antiviral; antibacterial;  
XX antifungal; gene therapy; diagnosis; membrane protein; protein secretion.

OS Homo sapiens.

PN MO200100824-A2.

PD 04-JAN-2001.

PF 16-JUN-2000; 2000MO-JP003944.

PR 24-JUN-1999; 99JP-00178065.

XX (SAGA ) SAGAMI CHEM RES CENT.  
XX (PROT-) PROTEGENE INC.

XX Kato S, Kilmura T;

DR WPI, 2001-123008/13.

DR N-PSDB; AAF30021.

XX New proteins with hydrophobic domains, useful for treating autoimmune  
XX diseases, inflammatory diseases, wounds, burns, incisions and ulcers.

XX Claim 1; Page 87-89; 126pp; English.

XX The present sequence is that of a novel human protein having a putative N  
XX -terminal secretory and transmembrane domain. It is predicted from cDNA  
XX clone HP03342 (see AAF30021). Isolated from a human umbilical cord blood  
XX cDNA library. The protein shows sequence similarity to Caenorhabditis  
XX elegans hypothetical protein CAA88972. The invention provides human  
XX proteins (see AAB20089-96) having hydrophobic domains indicative of  
XX secretory signals or membrane domains, and nucleic acids (see AAF30020-  
XX 27) encoding them. These are expected to have cell proliferation, cell  
XX differentiation, immunostimulant or immunosuppressor, haematopoiesis,  
XX regulating, tissue growth, activin, inhibin, chemotactic, chemokinetic,  
XX haemostatic, thrombolytic, receptor/ligand, antiinflammatory or  
XX antitumor activities (no evidence provided). Expression vectors,  
XX eukaryotic host cells and antibodies are also provided. The secreted or  
XX antigenic proteins of the invention can be used as pharmaceuticals or  
XX for preparing antibodies. Cells expressing them are utilized for  
XX detection of corresponding receptors or ligands, and in candidate drug  
XX screening

SQ Sequence 339 AA;

Query Match 100.0%; Score 1879; DB 4; Length 339;

Best Local Similarity 100.0%; Pred. No. 8.6e-162;

Matches 339; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAACGPGAGAGYCLILGLILFLTAGPALGMPDRMLADYKALTLHYDRYTSRRLLDP 60  
DB 1 MAACGPGAGAGYCLILGLILFLTAGPALGMPDRMLADYKALTLHYDRYTSRRLLDP 60  
QY 61 IPOLKCVGGTAGCDSTYTPKVIQCCKNGWDYDVQWECKTDLDIAYKFGKTVCCEGYESS 120  
DB 61 IPOLKCVGGTAGCDSTYTPKVIQCCKNGWDYDVQWECKTDLDIAYKFGKTVCCEGYESS 120  
QY 121 BDQYVARGSGCLEYVNDYTELGLQKLKESGKHGFASFSDYYTKMSADSCKNSGLITTV 180

DB 121 BDQYVARGSGCLEYVNDYTELGLQKLKESGKHGFASFSDYYTKMSADSCKNSGLITTV 180  
QY 181 VILGIAFVYTKFLSGGQYSPPPYSRHYRQFTNSAGPPPGFKEFTGPQNTGH 240  
DB 181 VILGIAFVYTKFLSGGQYSPPPYSRHYRQFTNSAGPPPGFKEFTGPQNTGH 240  
QY 241 GATSGFGSAFTGQGGYENSGPGFWTGLGTGGLIGYLFGSNRATPPSDSWYPSYSP 300  
DB 241 GATSGFGSAFTGQGGYENSGPGFWTGLGTGGLIGYLFGSNRATPPSDSWYPSYSP 300  
QY 301 GTWNRAYSPLHGGSGSYSCNSDTRKRTASGYGTRRR 339  
DB 301 GTWNRAYSPLHGGSGSYSCNSDTRKRTASGYGTRRR 339

## RESULT 7

AAM78498  
ID AAM78498 standard; protein; 339 AA.

AC AAM78498;

DT 06-NOV-2001 (first entry)

DE Human protein SEQ ID NO 1160.

XX Human; cytokine; cell proliferation; cell differentiation; gene therapy;  
XX vaccine; peptide therapy; stem cell growth factor; haematopoiesis;  
XX tissue growth factor; immunomodulatory; cancer; leukaemia;  
XX nervous system disorder; arthritis; inflammation.

OS Homo sapiens.

PN MO200157190-A2.

PD 09-AUG-2001.

PF 05-FEB-2001; 2001MO-US004098.

PR 03-FEB-2000; 2000US-00496914.

PR 27-APR-2000; 2000US-00560875.

PR 20-JUN-2000; 2000US-00598075.

PR 19-JUL-2000; 2000US-00620325.

PR 01-SEP-2000; 2000US-00654936.

PR 15-SEP-2000; 2000US-00663561.

PR 20-OCT-2000; 2000US-00693325.

PR 30-NOV-2000; 2000US-00728422.

XX (HYSR-) HYSRQ INC.

XX Tang YT, Liu C, Drmanac RT, Asundi V, Zhou P, Xu C, Cao Y;  
XX Ma Y, Zhao QA, Wang D, Wang J, Zhang J, Ren F, Chen R, Wang ZW;  
XX Xue AJ, Yang Y, Wejhrman T, Goodrich R;

DR WPI, 2001-476283/51.

DR N-PSDB; AAK51651.

XX Nucleic acids encoding polypeptides with cytokine-like activities, useful  
XX in diagnosis and gene therapy.

SQ Claim 20; Page 3398-3399; 6221pp; English.

XX The invention relates to polynucleotides (AAK51456-AAK53435) and the  
XX encoded polypeptides (AAM78323-AAK80302) that exhibit activity elating to  
XX cytokine, cell proliferation or cell differentiation or which may induce  
XX production of other cytokines in other cell populations. The  
XX polynucleotides and polypeptides are useful in gene therapy, vaccines or  
XX peptide therapy. The polypeptides have various cytokine-like activities,  
XX e.g. stem cell growth factor activity, haematopoiesis regulating  
XX activity, tissue growth factor activity, immunomodulatory activity and  
XX activin/inhibin activity and may be useful in the diagnosis and/or  
XX treatment of cancer, leukaemia, nervous system disorders, arthritis and  
XX inflammation. Note: Records for SEQ ID NO 2110 (AAK52581), 2111

CC (AAKS2582) and 3666 (AAM0020) are omitted as the relevant pages from the  
 CC sequence listing were missing at the time of publication

XX Sequence 339 AA;

Query Match 100.0%; Score 1879; DB 4; Length 339;  
 Best Local Similarity 100.0%; Pred. No. 8,6e-162;  
 Matches 339; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAACGPGAGYCLLGLHLFLITAGPALGMNDPDMLLRDVKALTLHYDRYTSRRLLP 60  
 DB 1 MAACGPGAGYCLLGLHLFLITAGPALGMNDPDMLLRDVKALTLHYDRYTSRRLLP 60  
 QY 61 IPOLKCVGAGCDSYTPKVIQCKNGMDGYDVQWCKCTDLDAKFKGVVSCGEYSS 120  
 DB 61 IPOLKCVGAGCDSYTPKVIQCKNGMDGYDVQWCKCTDLDAKFKGVVSCGEYSS 120  
 QY 121 EDQVYLRSGCGLEYNLDYTELGQLKESGKHGFASFSDDYKMSADSCKMSGILITIV 180  
 DB 121 EDQVYLRSGCGLEYNLDYTELGQLKESGKHGFASFSDDYKMSADSCKMSGILITIV 180  
 QY 121 EDQVYLRSGCGLEYNLDYTELGQLKESGKHGFASFSDDYKMSADSCKMSGILITIV 180  
 DB 121 EDQVYLRSGCGLEYNLDYTELGQLKESGKHGFASFSDDYKMSADSCKMSGILITIV 180  
 QY 181 VILGIAFVYVKLFLSDGQYSPPEYSEYPPFSHRVQRFNLSAGPPPGFKSEFTGPQNTGH 240  
 DB 181 VILGIAFVYVKLFLSDGQYSPPEYSEYPPFSHRVQRFNLSAGPPPGFKSEFTGPQNTGH 240  
 QY 241 GATSGFGSAFTGQGGYENSGPGFWTGLTGGLGVLFGSNRAATPDSWYPSYPSYP 300  
 DB 241 GATSGFGSAFTGQGGYENSGPGFWTGLTGGLGVLFGSNRAATPDSWYPSYPSYP 300  
 QY 301 GTMNRAVSPPLHGGSSGSYSVCSNSDITKTRTASGYGTRRR 339  
 DB 301 GTMNRAVSPPLHGGSSGSYSVCSNSDITKTRTASGYGTRRR 339

RESULT 8  
 AAU29275  
 ID AAU29275 standard; protein; 339 AA.  
 AC AAU29275;  
 XX 18-DEC-2001 (first entry)  
 DT Human PRO polypeptide sequence #252.  
 DE  
 XX PRO polypeptide; mammal; tumour; cancer; human; cattle; horse; sheep;  
 KM dog; cat; pig; goat; rabbit; tumour necrosis factor alpha; TNF-alpha;  
 KW blood; chondrocyte cell; cell proliferation; cell differentiation; colon;  
 KM adrenal; lung; breast; prostate; rectum; cervix; liver; genetic disorder.  
 OS Homo sapiens.  
 PN WO200168848-A2.  
 PD 20-SEP-2001.  
 XX 28-FEB-2001; 2001WO-US006520.  
 PF  
 XX 01-MAR-2000; 2000WO-US005601.  
 PR 02-MAR-2000; 2000WO-US005841.  
 PR 03-MAR-2000; 2000US-0187202P.  
 PR 06-MAR-2000; 2000US-0186968P.  
 PR 14-MAR-2000; 2000US-0189320P.  
 PR 14-MAR-2000; 2000US-0189328P.  
 PR 15-MAR-2000; 2000WO-US006884.  
 PR 21-MAR-2000; 2000US-0190828P.  
 PR 21-MAR-2000; 2000US-0191077P.  
 PR 21-MAR-2000; 2000US-0191048P.  
 PR 21-MAR-2000; 2000US-0191314P.  
 PR 28-MAR-2000; 2000US-0192855P.  
 PR 29-MAR-2000; 2000US-0193032P.  
 PR 30-MAR-2000; 2000WO-US008439.  
 PR 04-APR-2000; 2000US-0194449P.

PR 04-APR-2000; 2000US-0194647P.  
 PR 11-APR-2000; 2000US-0195975P.  
 PR 11-APR-2000; 2000US-0196000P.  
 PR 11-APR-2000; 2000US-0196187P.  
 PR 11-APR-2000; 2000US-0196690P.  
 PR 11-APR-2000; 2000US-0196690P.  
 PR 11-APR-2000; 2000US-0196820P.  
 PR 18-APR-2000; 2000US-0198121P.  
 PR 18-APR-2000; 2000US-0198585P.  
 PR 25-APR-2000; 2000US-0198397P.  
 PR 25-APR-2000; 2000US-0199550P.  
 PR 25-APR-2000; 2000US-0199654P.  
 PR 03-MAY-2000; 2000US-0201516P.  
 PR 17-MAY-2000; 2000WO-US013705.  
 PR 22-MAY-2000; 2000WO-US014042.  
 PR 30-MAY-2000; 2000WO-US014941.  
 PR 02-JUN-2000; 2000WO-US015264.  
 PR 05-JUN-2000; 2000US-0209832P.  
 PR 28-JUL-2000; 2000WO-US020710.  
 PR 22-AUG-2000; 2000US-00644848.  
 PR 24-AUG-2000; 2000WO-US023328.  
 PR 08-NOV-2000; 2000WO-US030952.  
 PR 01-DEC-2000; 2000WO-US032678.  
 PR 20-DEC-2000; 2000WO-US034956.  
 PA (GENTECH ) GENENTECH INC.  
 XX Baker KP, Chen J, Desnoyers L, Goddard A, Godowski PJ, Gurney AL;  
 PI Pan J, Smith V, Watanabe CK, Wood WI, Zhang Z;  
 DR WPI; 2001-602746/68.  
 XX N-PSDB; AAS46176.  
 PT Novel nucleic acids encoding PRO polypeptides, used to diagnose the  
 PT presence of tumors, such as prostate and breast tumors, in mammals and to  
 PT screen for modulators of the compounds.  
 XX  
 PS Claim 11; Fig 504; 774pp; English.  
 XX  
 CC Sequences AAU29024-AAU29328 represent PRO polypeptides of the invention.  
 CC The PRO polypeptides and their associated nucleic acids can be used to  
 CC detect the presence of a tumour in a mammal by comparing the level of  
 CC expression of a PRO polypeptide in a test sample of cells from the animal  
 CC and a control sample of normal cells, whereby a higher level of  
 CC expression in the test sample indicates the presence of a tumour in the  
 CC mammal. Mammals include dogs, cats, cattle, horses, sheep, pigs, goats  
 CC and rabbits but are preferably human. The polypeptides can be used to  
 CC stimulate tumour necrosis factor (TNF) alpha release from human blood,  
 CC when contacted with it. A specific polypeptide can be used to stimulate  
 CC the proliferation or differentiation of chondrocyte cells. The PRO  
 CC proteins can be used to determine the presence of tumours and also  
 CC susceptibility to tumour development, particularly adrenal, lung, colon,  
 CC breast, prostate, rectal, cervical, or liver tumours, in mammalian  
 CC subjects. The oligonucleotide probes specific for the PRO nucleic acids  
 CC can be used for genetic analysis of individuals with genetic disorders  
 XX  
 XX Sequence 339 AA;  
 SO  
 Query Match 100.0%; Score 1879; DB 4; Length 339;  
 Best Local Similarity 100.0%; Pred. No. 8,6e-162;  
 Matches 339; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAACGPGAGYCLLGLHLFLITAGPALGMNDPDMLLRDVKALTLHYDRYTSRRLLP 60  
 DB 1 MAACGPGAGYCLLGLHLFLITAGPALGMNDPDMLLRDVKALTLHYDRYTSRRLLP 60  
 QY 61 IPOLKCVGAGCDSYTPKVIQCKNGMDGYDVQWCKCTDLDAKFKGVVSCGEYSS 120  
 DB 61 IPOLKCVGAGCDSYTPKVIQCKNGMDGYDVQWCKCTDLDAKFKGVVSCGEYSS 120  
 QY 121 EDQVYLRSGCGLEYNLDYTELGQLKESGKHGFASFSDDYKMSADSCKMSGILITIV 180  
 DB 121 EDQVYLRSGCGLEYNLDYTELGQLKESGKHGFASFSDDYKMSADSCKMSGILITIV 180

QY 181 VLLGIAFVYVYKFLPSDQYSPPEYSEYPPSHRYORFTNSAGPPPGKSEFTGPONTGH 240  
 DB 181 VLLGIAFVYVYKFLPSDQYSPPEYSEYPPSHRYORFTNSAGPPPGKSEFTGPONTGH 240  
 QY 241 GATSGFGSAFTGQCGYENSGPGFWTGLGTGGIILYLFSGSNRAATPPSDSWYTPSPSP 300  
 DB 241 GATSGFGSAFTGQCGYENSGPGFWTGLGTGGIILYLFSGSNRAATPPSDSWYTPSPSP 300  
 QY 301 GTMNRAYSPLHGGSGSYVCSNSDPTKRTASGVGSTRR 339  
 DB 301 GTMNRAYSPLHGGSGSYVCSNSDPTKRTASGVGSTRR 339  
 RESULT 9  
 ID ABB84979 standard; protein; 339 AA.  
 AC ABB84979;  
 XX  
 DT 16-MAY-2002 (first entry)  
 XX  
 DE Human PRO4499 protein sequence SEQ ID NO:336.  
 XX  
 KW Human; angiogenesis; cardiac; cytoelastic; antiangiogenic; hypotensive;  
 KW vulnerability; antiarteriosclerotic; PRO agonist; PRO antagonist; trauma;  
 KW gene therapy; cardiovascular disorder; endothelial disorder; cancer;  
 KW angiogenic disorder; cardiac hypertrophy; atherosclerosis; hypertension;  
 KW age-related macular degeneration; arterial restenosis; angina;  
 KW rheumatoid arthritis; myocardial infarction; thrombophlebitis;  
 KW lymphangitis; tumour angiogenesis; breast carcinoma; liver carcinoma;  
 KW wound healing; chromosome mapping; gene mapping.  
 XX  
 OS Homo sapiens.  
 PN WO20020690-A2.  
 XX  
 PD 03-JAN-2002.  
 XX  
 PF 20-JUN-2001; 2001WO-US019692.  
 XX  
 PR 23-JUN-2000; 2000US-0213637P.  
 PR 20-JUL-2000; 2000US-0219556P.  
 PR 25-JUL-2000; 2000US-0220624P.  
 PR 25-JUL-2000; 2000US-0220664P.  
 PR 28-JUL-2000; 2000WO-US020710.  
 PR 02-AUG-2000; 2000US-0222659P.  
 PR 17-AUG-2000; 2000US-00643657.  
 PR 23-AUG-2000; 2000WO-US023328.  
 PR 24-AUG-2000; 2000WO-US023328.  
 PR 07-SEP-2000; 2000US-0230978P.  
 PR 18-SEP-2000; 2000US-0064610.  
 PR 18-SEP-2000; 2000US-0065350.  
 PR 24-OCT-2000; 2000US-0242922P.  
 PR 08-NOV-2000; 2000US-00709238.  
 PR 08-NOV-2000; 2000WO-US030952.  
 PR 10-NOV-2000; 2000WO-US030873.  
 PR 01-DEC-2000; 2000WO-US032678.  
 PR 20-DEC-2000; 2000US-00747259.  
 PR 20-DEC-2000; 2000WO-US034956.  
 PR 22-JAN-2001; 2001US-00767609.  
 PR 28-FEB-2001; 2001US-00796498.  
 PR 28-FEB-2001; 2001WO-US006520.  
 PR 01-MAR-2001; 2001WO-US006666.  
 PR 09-MAR-2001; 2001US-00802706.  
 PR 14-MAR-2001; 2001US-00808689.  
 PR 22-MAR-2001; 2001US-00816744.  
 PR 05-APR-2001; 2001US-00828366.  
 PR 10-MAY-2001; 2001US-00854208.  
 PR 10-MAY-2001; 2001US-00854280.  
 PR 25-MAY-2001; 2001US-00866028.  
 PR 25-MAY-2001; 2001US-00866034.  
 PR 25-MAY-2001; 2001WO-US017092.  
 PR 30-MAY-2001; 2001US-00870574.

PR 30-MAY-2001; 2001WO-US017443.  
 PR 01-JUN-2001; 2001WO-US017800.  
 XX  
 PA (GETH ) GENENTECH INC.  
 XX  
 PI Baker KP, Ferrara N, Gerber H, Gertlisen ME, Goddard A;  
 PI Godowski PJ, Gurney AL, Hillan KJ, Marsters SA, Pan J, Paoni NF;  
 PI Stephen JF, Matanabe CK, Williams PM, Wood WI, Ye W;  
 XX WPI; 2002-090516/12.  
 DR N-PSDB; ABL88234.  
 XX  
 PT One hundred and eighty seven nucleic acids encoding PRO polypeptides,  
 PT useful in diagnosis and treatment of cardiovascular (e.g. myocardial  
 PT infarction), endothelial or angiogenic disorders in a mammal.  
 XX  
 PS Claim 11; Fig 326; 565bp; English.  
 XX  
 CC ABL88072 to ABL88258 encode the PRO proteins given in ABB84817 to  
 CC ABB85003. The PRO proteins and polynucleotides have cardiac, cytoelastic,  
 CC antiangiogenic, hypotensive, vulnerability and antiarteriosclerotic  
 CC activities, and can be used in gene therapy. The PRO polynucleotides,  
 CC proteins, agonists and antagonists are useful for treating or diagnosing  
 CC a cardiovascular, endothelial or angiogenic disorder in a mammal, e.g.  
 CC cardiac hypertrophy, trauma, cancer, age-related macular degeneration,  
 CC atherosclerosis, hypertension, arterial restenosis, rheumatoid arthritis,  
 CC angina, myocardial infarctions, thrombophlebitis, lymphangitis, tumour  
 CC angiogenesis (such as breast carcinoma and liver carcinoma) and wound  
 CC healing. The PRO polynucleotides have applications in molecular biology,  
 CC including use as hybridization probes, and in chromosome and gene  
 CC mapping. ABL88259 to ABL88267 represent primers and probes used in the  
 CC exemplification of the present invention  
 XX  
 SQ Sequence 339 AA;  
 XX  
 Query Match 100.0%; Score 1879; DB 5; Length 339;  
 Best Local Similarity 100.0%; Pred. No. 8.6e-162;  
 Matches 339; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MAAACGPGAGYCLLGLHLFLITAGPALGMDPRLMDVYKALTLHYDRYTTSRRLDP 60  
 DB 1 MAAACGPGAGYCLLGLHLFLITAGPALGMDPRLMDVYKALTLHYDRYTTSRRLDP 60  
 QY 61 IPQLKCVGGTAGCDSTTPKVIQCONKMGYDVQMECTDLDIAYKFKTVSCGEYESS 120  
 DB 61 IPQLKCVGGTAGCDSTTPKVIQCONKMGYDVQMECTDLDIAYKFKTVSCGEYESS 120  
 QY 121 EDOYVLRGSGGLEYNLDYTELGLQKIKESGKOHGPFASFSYXYKWSADSCNMSGILITIV 180  
 DB 121 EDOYVLRGSGGLEYNLDYTELGLQKIKESGKOHGPFASFSYXYKWSADSCNMSGILITIV 180  
 QY 181 VLLGIAFVYVYKFLPSDQYSPPEYSEYPPSHRYORFTNSAGPPPGKSEFTGPONTGH 240  
 DB 181 VLLGIAFVYVYKFLPSDQYSPPEYSEYPPSHRYORFTNSAGPPPGKSEFTGPONTGH 240  
 QY 241 GATSGFGSAFTGQCGYENSGPGFWTGLGTGGIILYLFSGSNRAATPPSDSWYTPSPSP 300  
 DB 241 GATSGFGSAFTGQCGYENSGPGFWTGLGTGGIILYLFSGSNRAATPPSDSWYTPSPSP 300  
 QY 301 GTMNRAYSPLHGGSGSYVCSNSDPTKRTASGVGSTRR 339  
 DB 301 GTMNRAYSPLHGGSGSYVCSNSDPTKRTASGVGSTRR 339  
 RESULT 10  
 ID ABB61425 standard; protein; 339 AA.  
 AC ABB61425;  
 XX  
 DT 30-SEP-2002 (first entry)  
 XX  
 DE Human NF-kB activating protein SEQ ID NO 3.



CC useful in gene therapy, and as molecular weight markers for protein electrophoresis purposes. The sequences may also be used to detect overexpression on PRO polypeptides in cancerous tumours and for screening CC for differentially expressed genes using microarray technology. The CC present sequence represents a human PRO protein of the invention

XX Sequence 339 AA;

Query Match 100.0%; Score 1879; DB 5; Length 339;  
Best Local Similarity 100.0%; Pred. No. 8.6e-162; Mismatches 0; Gaps 0;  
Matches 339; Conservative 0; Indels 0;

QY 1 MAAACGPAAGYCYLLGLHLFLITAGPALGWNDDPMLRDVKALTLHYDRYTSRRLP 60  
DB 1 MAAACGPAAGYCYLLGLHLFLITAGPALGWNDDPMLRDVKALTLHYDRYTSRRLP 60  
QY 61 IPOLKCVGTAGCDSTTPKVIQCONKMGDGYDVOMECKTDIDIAVKEGKTIVSCEGYESS 120  
DB 61 IPOLKCVGTAGCDSTTPKVIQCONKMGDGYDVOMECKTDIDIAVKEGKTIVSCEGYESS 120  
QY 121 EDQVYVAGSGGLEYNLDYTELGLQKLBESGKHGPAPSPDYVYKMSADSCNMSGILITIV 180  
DB 121 EDQVYVAGSGGLEYNLDYTELGLQKLBESGKHGPAPSPDYVYKMSADSCNMSGILITIV 180  
QY 181 VLLGIATVYVYKLFPLSDGQYSPPYSEYPPFSHRVQFTNSAGPPPGFKSEFTGPONTGH 240  
DB 181 VLLGIATVYVYKLFPLSDGQYSPPYSEYPPFSHRVQFTNSAGPPPGFKSEFTGPONTGH 240  
QY 241 GATSGFSAFTGQGGYENSGPFWTGLGTGGLGLYLFSGNRAATPFSDSWYPSYPSYP 300  
DB 241 GATSGFSAFTGQGGYENSGPFWTGLGTGGLGLYLFSGNRAATPFSDSWYPSYPSYP 300  
QY 301 GTWNRAYSPLHGSGSYVCNSNSTKRTKRTASGYGCTRR 339  
DB 301 GTWNRAYSPLHGSGSYVCNSNSTKRTKRTASGYGCTRR 339

# RESULT 12

ABBS5585  
ID ABBS5585 standard; protein; 339 AA.

AC ABB95585;  
DT 19-JUL-2002 (first entry)

XX Human angiogenesis related protein PRO4499 SEQ ID NO: 326.

XX Human; angiogenesis; PRO protein; cardiovascularisation; wound; cancer;  
KM atherosclerosis; cardiac hypertrophy; gene therapy; endothelial disorder;  
KM cardiac; cytoskeletal; antiangiogenic; hypotensive; vulnerary;  
KM antiarteriosclerotic.

XX Homo sapiens.

XX WO200208284-A2.

XX 31-JAN-2002.

XX 09-JUL-2001; 2001WO-US021735.

XX 20-JUL-2000; 2000US-0219556P.

XX 25-JUL-2000; 2000US-0220624P.

XX 25-JUL-2000; 2000US-022064P.

XX 28-JUL-2000; 2000WO-US020710.

XX 02-AUG-2000; 2000US-0222695P.

XX 17-AUG-2000; 2000US-00643657.

XX 23-AUG-2000; 2000WO-US023522.

XX 24-AUG-2000; 2000WO-US023328.

XX 07-SEP-2000; 2000US-0230978P.

XX 18-SEP-2000; 2000US-0064610.

XX 18-SEP-2000; 2000US-0066530.

XX 24-OCT-2000; 2000US-0242922P.

XX 08-NOV-2000; 2000US-00709238.

PR 08-NOV-2000; 2000WO-US030952.  
PR 10-NOV-2000; 2000WO-US030873.  
PR 01-DEC-2000; 2000WO-US032578.  
PR 20-DEC-2000; 2000US-00747259.  
PR 20-DEC-2000; 2000WO-US034956.  
PR 22-JAN-2001; 2001US-00767609.  
PR 28-FEB-2001; 2001US-00796498.  
PR 28-FEB-2001; 2001WO-US006520.  
PR 01-MAR-2001; 2001WO-US006666.  
PR 09-MAR-2001; 2001US-00802706.  
PR 14-MAR-2001; 2001US-00808689.  
PR 22-MAR-2001; 2001US-00816744.  
PR 05-APR-2001; 2001US-00828366.  
PR 10-MAY-2001; 2001US-00854208.  
PR 10-MAY-2001; 2001US-00854280.  
PR 25-MAY-2001; 2001US-00866028.  
PR 25-MAY-2001; 2001US-00866034.  
PR 25-MAY-2001; 2001WO-US017092.  
PR 30-MAY-2001; 2001US-00870574.  
PR 30-MAY-2001; 2001WO-US017443.  
PR 01-JUN-2001; 2001WO-US017800.  
PR 20-JUN-2001; 2001WO-US019692.

XX (GENT) GENENTECH INC.  
PA (BAKE/) BAKER K P.  
PA (ERRR) FERRARA N.  
PA (GERR/) GERBER H.  
PA (GERR/) GERRITSEN M E.  
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PA (GODO/) GODOWSKI P J.  
PA (GURN/) GURNEY A L.  
PA (HILL/) HILLAN K J.  
PA (MARS/) MASTERS S A.  
PA (PAND/) PAN J.  
PA (PAON/) PAONI N F.  
PA (STEP/) STEPHAN J F.  
PA (WATA/) WATANABE C K.  
PA (WILL/) WILLIAMS P M.  
PA (WOOD/) WOOD W I.

XX Baker KP, Ferrara N, Gerber H, Gerritsen ME, Goddard A;  
PI Godowski PJ, Gurney AL, Hillan KJ, Mareters SA, Pan J, Paoni NF;  
PI Stephan JF, Watanabe CK, Williams PM, Wood WI, Ye W;  
XX WPI, 2002-171999/22.  
XX N-PDB; ABL95723.

XX One hundred and eighty seven nucleic acids encoding PRO polypeptides,  
PT useful in diagnosis and treatment of cardiovascular (e.g. myocardial  
PT infarction), endothelial or angiogenic disorders in a mammal.

XX Claim 11; Fig 326; 567pp; English.

XX The present invention provides the protein and coding sequences of human  
XX PRO proteins. These are useful for treating or diagnosing a  
XX cardiovascular, endothelial or angiogenic disorder, including cardiac  
XX hypertrophy, trauma, cancer, age-related macular degeneration,  
XX atherosclerosis, hypertension, arterial stenosis, rheumatoid arthritis,  
XX angina, myocardial infarctions, thrombophlebitis, lymphangitis, tumour  
XX angiogenesis (such as breast carcinoma and liver carcinoma) and wound  
XX healing. The present sequence is a PRO protein of the invention

XX Sequence 339 AA;

Query Match 100.0%; Score 1879; DB 5; Length 339;  
Best Local Similarity 100.0%; Pred. No. 8.6e-162; Mismatches 0; Gaps 0;  
Matches 339; Conservative 0; Indels 0;

QY 1 MAAACGPAAGYCYLLGLHLFLITAGPALGWNDDPMLRDVKALTLHYDRYTSRRLP 60  
DB 1 MAAACGPAAGYCYLLGLHLFLITAGPALGWNDDPMLRDVKALTLHYDRYTSRRLP 60  
QY 61 IPOLKCVGTAGCDSTTPKVIQCONKMGDGYDVOMECKTDIDIAVKEGKTIVSCEGYESS 120

DB 61 IPOLKCVGAGTACDSTYTPKVIQCONKGMWDYDVQWECKTDLDAVYFGKTVSCGEYESS 120  
QY 121 EDQYVLRGSGLEBNLDYTELGLOKLKESGKHGFASFSYVYKWSADSCNMSGILITTV 180  
DB 121 EDQYVLRGSGLEBNLDYTELGLOKLKESGKHGFASFSYVYKWSADSCNMSGILITTV 180  
QY 181 VLLGIAFVYVYKFLFSDGQYSPPEYSEYPPSHRYORFTNSAGPPPGFKSEFTGQNTGH 240  
DB 181 VLLGIAFVYVYKFLFSDGQYSPPEYSEYPPSHRYORFTNSAGPPPGFKSEFTGQNTGH 240  
QY 241 GATSGFGSAFTGQGGYENSGPGFWTGLGTGIGILYFGSNRAATPPSDSWYTPSPSY 300  
DB 241 GATSGFGSAFTGQGGYENSGPGFWTGLGTGIGILYFGSNRAATPPSDSWYTPSPSY 300  
QY 301 GTWNRAYSPLHGGSGSYVCSNSDTKTRTASGYGTRRR 339  
DB 301 GTWNRAYSPLHGGSGSYVCSNSDTKTRTASGYGTRRR 339

## RESULT 13

ABP61841 standard; protein; 339 AA.

AC ABP61841;  
DT 04-OCT-2002 (first entry)

DE Human polypeptide SEQ ID NO 195.

XX Human; cytostatic; antirheumatic; antiarthritic; vulnery; analgesic;  
XX antiinflammatory; antibacterial; immunosuppressive; antiparkinsonian;  
XX neuroprotective; nootropic; osteopathic; haemostatic; vasoconstrictive;  
XX anticancer; fungicide; antidiabetic; antiaesthetic; antiallergic;  
XX immunostimulant; antiparasitic; secreted protein; transmembrane protein;  
XX cytokine; cell proliferation; cell differentiation; neurotrophic;  
XX stem cell; growth factor; nervous system disease; Huntington's disease;  
XX Alzheimer's disease; Parkinson's disease; Huntington's disease;  
XX osteoporosis; severe combined immunodeficiency; SCID; infection;  
XX multiple sclerosis; rheumatoid arthritis; gene therapy.

OS Homo sapiens.

XX US2002065394-A1.

PD 30-MAY-2002.

XX 22-DEC-2000; 2000US-00745763.

XX 18-MAR-1998; 98US-00040963.

XX (JACO/) JACOBS K.  
XX (MCCO/) MCCOY J M.  
XX (LAVA/) LAVALLIE E R.  
XX (COLL/) COLLINS-RACIE L A.  
XX (EVAN/) EVANS C.  
XX (MERB/) MERBERG D.  
XX (TREB/) TREACY M.  
XX (SPAU/) SPAULDING V.

XX Jacobs K, McCoy JM, Lavallie ER, Collins-Racie LA, Evans C;  
XX Merberg D, Treacy M, Spaulding V;  
XX MPI: 2002-582343/62.  
XX N-PSDB; ABQ92055.

XX Novel secreted or transmembrane protein and polynucleotide encoding the  
XX protein, useful for diagnosis and treatment of neurological disorders,  
XX cancer, autoimmune diseases, bone disorders and lung or liver fibrosis.

XX Claim 184; Page 193; 284pp; English.

XX The invention relates to human secreted or transmembrane protein (I),

CC their fragments and is encoded by specific complementary deoxyribonucleic  
CC acid (cDNA) inserts (II), where the protein is substantially free from  
CC other mammalian proteins. (I) are useful for preventing, treating or  
CC ameliorating a medical condition, especially immunological treatment or  
CC prevention of tumors. (I) exhibits activity relating to angiogenesis,  
CC cytokine, cell proliferation, cell differentiation, antiinflammatory,  
CC stem cell growth factor activity and activin or inhibin-related  
CC activities. (I) can be used to manipulate stem cells in culture to give  
CC rise to neuroepithelial cells that can be used to augment or replace  
CC cells damaged by illness, autoimmune disease, accidental damage or  
CC genetic disorders. (I) induces the proliferation of neural cells and  
CC regeneration of nerve and brain tissue and is useful for the treatment of  
CC central and peripheral nervous system diseases and neuropathies, such as  
CC Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic  
CC lateral sclerosis. (I) is involved in chemotactic or chemokinetic  
CC activity, regulation of haematopoiesis and is useful for treating myeloid  
CC or lymphoid cell disorders, platelet disorders such as thrombocytopenia  
CC and for regeneration of bone, cartilage, tendon, ligament and/or nerve  
CC tissue growth and in tissue repair, healing of burns, incisions, ulcers,  
CC for treating osteoporosis, osteoarthritis, bone degenerative disorders or  
CC periodontal disease. (I) is also useful for gut protection or  
CC regeneration and treatment of lung or liver fibrosis, reperfusion injury  
CC in various tissues, various immune deficiencies and disorders including  
CC severe combined immunodeficiency (SCID), bacterial or fungal infections,  
CC autoimmune disorders e.g. multiple sclerosis, rheumatoid arthritis,  
CC diabetes mellitus, myasthenia gravis, allergic reactions and conditions,  
CC such as asthma or other respiratory problems. (II) is useful to express  
CC recombinant protein, as markers for tissues in which the corresponding  
CC protein is preferentially expressed and in gene therapy. The present  
CC sequence is that of a polypeptide of the invention

XX Sequence 339 AA;

XX Query Match 100.0%; Score 1879; DB 5; Length 339;

XX Best Local Similarity 100.0%; Pred. No. 8.6e-162; Indels 0; Gaps 0;

XX Matches 339; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAACGPGAGYCLLGLHLFTLTAGPALGMWDPRLRLDVKALTLHYDRYTSRRIDP 60

DB 1 MAACGPGAGYCLLGLHLFTLTAGPALGMWDPRLRLDVKALTLHYDRYTSRRIDP 60

QY 61 IPOLKCVGAGTACDSTYTPKVIQCONKGMWDYDVQWECKTDLDAVYFGKTVSCGEYESS 120

DB 61 IPOLKCVGAGTACDSTYTPKVIQCONKGMWDYDVQWECKTDLDAVYFGKTVSCGEYESS 120

QY 121 EDQYVLRGSGLEBNLDYTELGLOKLKESGKHGFASFSYVYKWSADSCNMSGILITTV 180

DB 121 EDQYVLRGSGLEBNLDYTELGLOKLKESGKHGFASFSYVYKWSADSCNMSGILITTV 180

QY 181 VLLGIAFVYVYKFLFSDGQYSPPEYSEYPPSHRYORFTNSAGPPPGFKSEFTGQNTGH 240

DB 181 VLLGIAFVYVYKFLFSDGQYSPPEYSEYPPSHRYORFTNSAGPPPGFKSEFTGQNTGH 240

QY 241 GATSGFGSAFTGQGGYENSGPGFWTGLGTGIGILYFGSNRAATPPSDSWYTPSPSY 300

DB 241 GATSGFGSAFTGQGGYENSGPGFWTGLGTGIGILYFGSNRAATPPSDSWYTPSPSY 300

QY 301 GTWNRAYSPLHGGSGSYVCSNSDTKTRTASGYGTRRR 339

DB 301 GTWNRAYSPLHGGSGSYVCSNSDTKTRTASGYGTRRR 339

## RESULT 14

ABU58651 standard; protein; 339 AA.

XX ABU58651;

XX 15-APR-2003 (first entry)

XX Human PRO polypeptide #252.

XX Human; cytostatic; tumour; cancer; breast; lung; stomach; liver;

KM	dog, cat, cow, horse, sheep, pig, goat, rabbit, ADAPT; antibody-dependent enzyme mediated prodrgng therapy.	PR	04-JUN-1998;	98US-0088025P
KK		PR	04-JUN-1998;	98US-0088028P
XX		PR	04-JUN-1998;	98US-0088029P
XX		PR	04-JUN-1998;	98US-0088033P
XX		PR	04-JUN-1998;	98US-0088036P
XX		PR	05-JUN-1998;	98US-0088167P
XX		PR	05-JUN-1998;	98US-0088202P
XX		PR	05-JUN-1998;	98US-0088212P
XX		PR	05-JUN-1998;	98US-0088217P
XX		PR	09-JUN-1998;	98US-0088655P
XX		PR	10-JUN-1998;	98US-0088722P
XX		PR	10-JUN-1998;	98US-0088738P
XX		PR	10-JUN-1998;	98US-0088740P
XX		PR	10-JUN-1998;	98US-0088811P
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XX		PR	10-JUN-1998;	98US-0088825P
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XX		PR	16-JUN-1998;	98US-0089514P
XX		PR	17-JUN-1998;	98US-0089538P
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XX		PR	17-JUN-1998;	98US-0089653P
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XX		PR	19-JUN-1998;	98US-0089952P
XX		PR	22-JUN-1998;	98US-0090246P
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PR 26-AUG-1998; 98US-0098014P.  
PR 01-SRP-1998; 98US-0098716P.  
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PR 02-SRP-1998; 98US-0098803P.  
PR 02-SRP-1998; 98US-0098821P.  
PR 02-SRP-1998; 98US-0098843P.  
PR 09-SRP-1998; 98US-0099602P.  
PR 10-SRP-1998; 98US-0099741P.  
PR 10-SRP-1998; 98US-0099754P.  
PR 10-SRP-1998; 98US-0099763P.  
PR 10-SRP-1998; 98US-0099812P.  
PR 15-SRP-1998; 98US-0100388P.  
PR 16-SRP-1998; 98US-0100662P.  
PR 16-SRP-1998; 98US-0100664P.  
PR 16-SRP-1998; 98US-0101751P.  
PR 16-SRP-1998; 98US-0101751P.  
PR 17-SRP-1998; 98US-0100683P.  
PR 17-SRP-1998; 98US-0100684P.  
PR 17-SRP-1998; 98US-0100919P.  
PR 18-SRP-1998; 98US-0100930P.  
PR 18-SRP-1998; 98US-0100949P.  
PR 18-SRP-1998; 98US-0101014P.  
PR 18-SRP-1998; 98US-0101068P.  
PR 23-SRP-1998; 98US-0101471P.  
PR 23-SRP-1998; 98US-0101472P.  
PR 23-SRP-1998; 98US-0101475P.  
PR 23-SRP-1998; 98US-0101477P.  
PR 24-SRP-1998; 98US-0101738P.  
PR 24-SRP-1998; 98US-0101739P.  
PR 24-SRP-1998; 98US-0101743P.  
PR 24-SRP-1998; 98US-0101922P.  
PR 25-SRP-1998; 98US-0101922P.  
PR 25-SRP-1998; 98US-0101786P.  
PR 29-SRP-1998; 98US-0102207P.  
PR 29-SRP-1998; 98US-0102240P.  
PR 29-SRP-1998; 98US-0102330P.  
PR 29-SRP-1998; 98US-0102331P.  
PR 30-SRP-1998; 98US-0102487P.  
PR 30-SRP-1998; 98US-0102570P.  
PR 30-SRP-1998; 98US-0102571P.  
PR 30-SRP-1998; 98US-0102684P.  
PR 01-OCT-1998; 98US-0102687P.  
PR 01-OCT-1998; 98US-0102687P.  
PR 02-OCT-1998; 98US-0102965P.  
PR 06-OCT-1998; 98US-0103458P.  
PR 06-OCT-1998; 98US-0103459P.  
PR 07-OCT-1998; 98US-00168978.

Query Match 100.0%; Score 1879; DB 6; Length 339;  
Best Local Similarity 100.0%; Pred. No. 8,6e-162;

Matches 339; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAACGPGAGCYCLLGLHIFLLTAGPALGMDPDMLADYKALTLHYDRTTSRLDP 60  
DB 1 MAACGPGAGCYCLLGLHIFLLTAGPALGMDPDMLADYKALTLHYDRTTSRLDP 60  
QY 61 IPOLKCVGAGTACDSTYPKVIQCONKGMDDYDVQMECKTDLDIAYKFKTVSCEGYESS 120  
DB 61 IPOLKCVGAGTACDSTYPKVIQCONKGMDDYDVQMECKTDLDIAYKFKTVSCEGYESS 120  
QY 121 EDQYVIRGSCGLEBYNLDYTELGLQKLKESGKHGPASFSDDYKWSADSCKNSGLITTV 180  
DB 121 EDQYVIRGSCGLEBYNLDYTELGLQKLKESGKHGPASFSDDYKWSADSCKNSGLITTV 180  
QY 181 VLLGLAFVYVKFLPSGQVSPRPYSEYPPSHRYQRTNAGPPPGFSEFTGPONTGH 240  
DB 181 VLLGLAFVYVKFLPSGQVSPRPYSEYPPSHRYQRTNAGPPPGFSEFTGPONTGH 240  
QY 241 GATSGFGSALFTGQOQYGENSGPGFWTGLGTGILGLYFGSRRATPPSDSWYTPSPSY 300  
DB 241 GATSGFGSALFTGQOQYGENSGPGFWTGLGTGILGLYFGSRRATPPSDSWYTPSPSY 300  
QY 301 GTWNRAYSPLHGGSGSYVCSNSDITKRTNAGYGTTRRR 339  
DB 301 GTWNRAYSPLHGGSGSYVCSNSDITKRTNAGYGTTRRR 339

RESULT 15  
ABU88199  
ID ABU88199 standard; protein; 339 AA.  
XX  
AC ABU88199;  
XX  
DT 07-JUL-2003 (first entry)  
XX  
DE Novel human secreted and transmembrane protein PRO4499.  
XX  
KW Human; secreted and transmembrane protein: PRO; gene therapy;  
KW tumour necrosis factor-alpha release; TNF-alpha release;  
KW chondrocyte proliferation; chondrocyte differentiation; tumour;  
KW adrenal tumour; lung tumour; colon tumour; breast tumour;  
KW prostate tumour; rectal tumour; cervical tumour; liver tumour.  
XX  
OS Homo sapiens.  
XX  
PN US2003032127-A1.  
XX  
PD 13-FEB-2003.  
XX  
PF 26-JUN-2002; 2002US-00183012.  
XX  
PR 18-SEP-1997; 97US-0059263P.  
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PR 17-OCT-1997; 97US-0062250P.  
PR 21-OCT-1997; 97US-0063486P.  
PR 24-OCT-1997; 97US-0063120P.  
PR 24-OCT-1997; 97US-0063121P.  
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PR 28-OCT-1997; 97US-0063544P.  
PR 28-OCT-1997; 97US-0063564P.  
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PR 31-OCT-1997; 97US-0063870P.  
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PR 11-DEC-1997; 97US-0069335P.  
PR 12-DEC-1997; 97US-0069425P.  
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PR 05-MAY-1998; 98US-0084366P.  
PR 06-MAY-1998; 98US-0084414P.



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PR 07-MAY-1998; 98US-0084639P.
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PR 07-MAY-1998; 98US-0084643P.
PR 15-MAY-1998; 98US-0085579P.
PR 15-MAY-1998; 98US-0085580P.
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PR 18-MAY-1998; 98US-0086023P.
PR 22-MAY-1998; 98US-0086392P.
PR 22-MAY-1998; 98US-0086486P.
PR 28-MAY-1998; 98US-0087038P.
PR 28-MAY-1998; 98US-0087208P.
PR 02-JUN-1998; 98US-0087609P.
PR 03-JUN-1998; 98US-0087759P.
PR 04-JUN-1998; 98US-0087837P.
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PR 11-JUN-1998; 98US-0088863P.
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PR 12-JUN-1998; 98US-0089090P.
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PR 17-JUN-1998; 98US-0089588P.
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PR 18-JUN-1998; 98US-0089653P.
PR 18-JUN-1998; 98US-0089908P.
PR 19-JUN-1998; 98US-0089952P.
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PR 10-AUG-1998; 98US-0095998P.
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PR 17-AUG-1998; 98US-0096757P.
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Best Local Similarity 100.0%; Pred. No. 8, 6e-162;
Matches 339; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy	241	GATSGFGSAFTGQGGYENSGBPFWTGLGTGILGYLFGSNRAATPPSDSMYPSYPSTP	300
Db	241	GATSGFGSAFTGQGGYENSGBPFWTGLGTGILGYLFGSNRAATPPSDSMYPSYPSTP	300
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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: July 14, 2005, 20:16:41 ; Search time 102.864 Seconds  
(without alignments)  
1273.204 Million cell updates/sec

Title: US-10-019-151C-2

Perfect score: 1879

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Scoring table: BIOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1726220 seqs, 386332138 residues

Total number of hits satisfying chosen parameters: 1726220

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Database : Listing first 45 summaries

Published Applications AA:\*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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2	1879	100.0	339	10 US-09-931-836-80	Sequence 80, App
3	1879	100.0	339	13 US-10-036-342-80	Sequence 80, App
4	1879	100.0	339	13 US-10-052-585-504	Sequence 504, App
5	1879	100.0	339	13 US-10-036-041-80	Sequence 80, App
6	1879	100.0	339	14 US-10-035-855-80	Sequence 80, App
7	1879	100.0	339	14 US-10-174-590-504	Sequence 504, App
8	1879	100.0	339	14 US-10-176-758-504	Sequence 504, App
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45	1879	100.0	339	14 US-10-174-576-504	Sequence 504, App

#### ALIGNMENTS

RESULT 1  
US-09-745-763-146  
Sequence 146, Application US/09745763  
Patent No. US20020065394A1

GENERAL INFORMATION:  
APPLICANT: Jacobs, Kenneth  
McCoy, John M.  
Lavallee, Edward R.  
Collins-Racle, Lisa A.  
Evans, Cheryl  
Metberg, David  
Treacy, Maurice  
Spaulding, Vikki

TITLE OF INVENTION: SECRETED PROTEINS AND POLYPEPTIDES  
ENCODING THEM

NUMBER OF SEQUENCES: 219

CORRESPONDENCE ADDRESS:  
ADDRESSER: Genetics Institute, Inc.  
STREET: 87 Cambridgepark Drive  
CITY: Cambridge  
STATE: MA  
COUNTRY: U.S.A.  
ZIP: 02140

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.30

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/745,763  
FILING DATE: 18-Jun-2000  
CLASSIFICATION: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: Sprunger, Suzanne A.

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/      REGISTRATION NUMBER: 41,323
/      TELECOMMUNICATION INFORMATION:
/      TELEPHONE: (617) 498-8284
/      TELEFAX: (617) 876-5851
/      INFORMATION FOR SEQ ID NO: 146:
/      SEQUENCE CHARACTERISTICS:
/      LENGTH: 339 amino acids
/      TYPE: amino acid
/      STRANDEDNESS: <unknown>
/      TOPOLOGY: linear
/      MOLECULE TYPE: protein
/      SEQUENCE DESCRIPTION: SEQ ID NO: 146:
US-09-745-763-146

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Matches 339; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 2
US-09-931-836-80
/      Sequence 80, Application US/09911836
/      Publication No. US20030027249A1
/      GENERAL INFORMATION:
/      APPLICANT: Deenoyers, Inc
/      APPLICANT: Baton, Dan L.
/      APPLICANT: Goddard, Audrey
/      APPLICANT: Godowski, Paul J.
/      APPLICANT: Gurney, Austin L.
/      APPLICANT: Pan, James
/      APPLICANT: Stewart, Timothy A.
/      APPLICANT: Watanabe, Colin K.
/      APPLICANT: Wood, William I.
/      APPLICANT: Zhang, Zhenlin
/      TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
/      FILE REFERENCE: P3030R1C1
/      CURRENT APPLICATION NUMBER: US/09/931,836
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/      PRIOR APPLICATION NUMBER: 60/085579
/      PRIOR FILING DATE: 1998-05-15
/      PRIOR APPLICATION NUMBER: 60/112514
/      PRIOR FILING DATE: 1998-12-15
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/      PRIOR APPLICATION NUMBER: PCT/US00/05601
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/ PRIOR APPLICATION NUMBER: PCT/US00/15264
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/ PRIOR APPLICATION NUMBER: PCT/US00/23328
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/ PRIOR FILING DATE: 2001-08-28
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/ PRIOR FILING DATE: 2001-06-01
/ PRIOR APPLICATION NUMBER: PCT/US01/19692
/ PRIOR FILING DATE: 2001-06-20
/ PRIOR APPLICATION NUMBER: PCT/US01/21066
/ PRIOR FILING DATE: 2001-06-29
/ PRIOR APPLICATION NUMBER: PCT/US01/21735
/ PRIOR FILING DATE: 2001-07-09
/ NUMBER OF SEQ ID NOS: 80
/ SEQ ID NO 80
/ LENGTH: 339
/ TYPE: PRT
/ ORGANISM: Homo Sapien
US-09-931-836-80
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Query Match 100.0%; Score 1879; DB 10; Length 339;
Best Local Similarity 100.0%; Pred. No. 4e-165;
Matches 339; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 181 VLLGLAFVYVKLPLSDGOYSPPPYSRYPFPHRYORFTNSAGPPPGFKSEFTGPQNTGH 240
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/ Sequence 80, Application US/10036342
/ Publication No. US20020090681A1
/ GENERAL INFORMATION:
/ APPLICANT: Deenoeyer, Luc
/ APPLICANT: Baton, Dan L.
/ APPLICANT: Goddard, Audrey
/ APPLICANT: Godowski, Paul J.
/ APPLICANT: Gurney, Austin L.
/ APPLICANT: Pan, James
/ APPLICANT: Stewart, Timothy A.
/ APPLICANT: Watanabe, Colin K.
/ APPLICANT: Wood, William I.
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```
/ APPLICANT: Zhang, Zhenli
/ TITLE OR INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
/ FILE REFERENCES: P3030RIC5
/ CURRENT APPLICATION NUMBER: US/10/036,342
/ PRIOR APPLICATION NUMBER: 2001-12-26
/ PRIOR FILING DATE: 1998-05-15
/ PRIOR APPLICATION NUMBER: 60/112514
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/ PRIOR APPLICATION NUMBER: 09/854208
/ PRIOR FILING DATE: 2001-05-10
/ PRIOR APPLICATION NUMBER: 09/854280
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; PRIOR APPLICATION NUMBER: PCT/US01/21735
; PRIOR FILING DATE: 2001-07-09
; NUMBER OF SEQ ID NOS: 80
; SEQ ID NO 80
; LENGTH: 339
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-036-342-80

Query Match      100.0%; Score 1879; DB 13; Length 339;
Best Local Similarity 100.0%; Pred. No. 4e-165;
Matches 339; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB      1  MAACGPGAGCYLGLGLHFLITAGPALGMDPDMRLRDVYKALTLHYDRYTSRLRP 60
QY      61  IPOLKCVGAGTCDSTYTPKVIQCONKMGDGYDVQWCKTDLDIAYKFGKTVVSCGEYESS 120
DB      61  IPOLKCVGAGTCDSTYTPKVIQCONKMGDGYDVQWCKTDLDIAYKFGKTVVSCGEYESS 120
QY      121  EDGYVLRGSGCLGELNLDYTELGLQKLESGKQGFAPSPDYTKKMSADSCKMSGLITTV 180
DB      121  EDGYVLRGSGCLGELNLDYTELGLQKLESGKQGFAPSPDYTKKMSADSCKMSGLITTV 180
QY      121  EDGYVLRGSGCLGELNLDYTELGLQKLESGKQGFAPSPDYTKKMSADSCKMSGLITTV 180
DB      121  EDGYVLRGSGCLGELNLDYTELGLQKLESGKQGFAPSPDYTKKMSADSCKMSGLITTV 180
QY      181  VLLGLAFVYVKLFLSDGQYSPPYSHYQFPTNSAGPPPGFSEFTGPONTGH 240
DB      181  VLLGLAFVYVKLFLSDGQYSPPYSHYQFPTNSAGPPPGFSEFTGPONTGH 240
QY      241  GATSGFGSAFTGQOQYENSGPGFWTGLGTGILGYLFGSNRAATPFSDSYTPSPSPY 300
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RESULT 4
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; Sequence 504, Application US/10052586
; Publication No. US20020127584A1
GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gueney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3430R1C1
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PRIOR FILING DATE: 1998-06-17  
PRIOR APPLICATION NUMBER: 60/089908

Query Match 100.0%; Score 1879; DB 13; Length 339;  
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QY 1 MAACGPGAGYCTLLGLHLFLTTAGPALGMDPDMTLRDVYALTLHYDRYTTSSRLDP 60  
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QY 61 IPOLKCYGAGTACDSTTPKVIQCONKGMGSDYDQMECKTDLDIAYKFGKTVSCBEGYSS 120  
DB 61 IPOLKCYGAGTACDSTTPKVIQCONKGMGSDYDQMECKTDLDIAYKFGKTVSCBEGYSS 120  
QY 121 BDQYVVRGSGLEYNLDYBELGQKLKESGKHGFASPSDYXXKMSADSNNSGLITTY 180  
DB 121 BDQYVVRGSGLEYNLDYBELGQKLKESGKHGFASPSDYXXKMSADSNNSGLITTY 180

Db 121 EDOYVLRGSGCLERYNDYTELGQKESGKHGFASPSDYKWSADSCKNSGLITTV 180  
QY 181 VLLGLAFVYKLTPLSDGQSPPEYSEYPPSHRYORFTNSAGPPPGFKSEFTGPONTG 240  
Db 181 VLLGLAFVYKLTPLSDGQSPPEYSEYPPSHRYORFTNSAGPPPGFKSEFTGPONTG 240  
QY 241 GATSGFSAFTGQOQYENSGPGFWTGLGTGILGYLFGSNRATPPSDSNVYSPSPSP 300  
Db 241 GATSGFSAFTGQOQYENSGPGFWTGLGTGILGYLFGSNRATPPSDSNVYSPSPSP 300  
QY 301 GTWNRAYSPLHGSGSYVCSNBDYTRTINAGYGTGRRR 339  
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RESULT 5  
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Sequence 80, Application US/10036041  
GENERAL INFORMATION:  
APPLICANT: DeNovo, Inc  
APPLICANT: Eaton, Dan L.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Guiney, Austin L.  
APPLICANT: Pan, James  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Watanabe, Colin K.  
APPLICANT: Wood, William I.  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
FILE OF INVENTION: ACIDS ENCODING THE SAME  
FILE REFERENCE: P3030R1C8  
CURRENT APPLICATION NUMBER: US/10/036, 041  
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PRIOR APPLICATION NUMBER: 09/908, 827  
PRIOR FILING DATE: 2001-07-18  
PRIOR APPLICATION NUMBER: PCT/US99/10733  
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PRIOR FILING DATE: 2001-07-09  
NUMBER OF SEQ ID NOS: 80  
SEQ ID NO 80  
LENGTH: 339  
TYPE: PRT  
ORGANISM: Homo Sapien



US-10-036-041-80

Query Match	100.0%	Score 1879;	DB 13;	length 339;
Best Local Similarity	100.0%	Pred. No. 4e-165;		
Matches 339; Conservative	0;	Mismatches	0;	Indels 0; Gaps 0;

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Qy	121	BDQYVLRGSGLEYNLDYTELGLOKLKESGKHGPASFSDYYKKMSADSQMSGLITIV	180
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Db	181	VLLGIAFVYYKFLPSGQGYSPPPSYRYPFPHSRYORFTNSAGPPPGKSEFTGPQNTGH	240
Qy	241	GATSGAGSAFTGGQGYENSGRGFTTGLGTGGILGLFSGNSAAATPSSSWYTPSPSPYP	300
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RESULT 6  
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: PRIOR FILING DATE: 2001-02-28
: PRIOR APPLICATION NUMBER: PCT/US01/17800
: PRIOR FILING DATE: 2001-06-01
: PRIOR APPLICATION NUMBER: PCT/US01/19692
: PRIOR FILING DATE: 2001-06-20
: PRIOR APPLICATION NUMBER: PCT/US01/21066
: PRIOR FILING DATE: 2001-06-29
: PRIOR APPLICATION NUMBER: PCT/US01/21735
: PRIOR FILING DATE: 2001-07-09
: NUMBER OF SEQ ID NOS: 80
: SEQ ID NO: 80
: LENGTH: 339
: TYPE: PRT
: ORGANISM: Homo Sapien
US-10-035-855-80

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Query Match	100.0%	Score 1879;	DB 14;	Length 339;
Best Local Similarity	100.0%	Pred. No. 4e-165;		
Matches 339;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

Qy 1 MAACGCGAAGCCLLIGHLFLITAGPALGWNDEDMRLADVKALTLHYRYTTSRRDP 600

Db 1 MAACGCGAAGCCLLIGHLFLITAGPALGWNDEDMRLADVKALTLHYRYTTSRRDP 600

Qy 61 I P Q L K C V G G T A G C D S Y T P K V I Q C Q N K M D G Y V Q M E C T D L D I A Y R K G K T V S C E G Y E S S 120

Db 61 I P Q L K C V G G T A G C D S Y T P K V I Q C Q N K M D G Y V Q M E C T D L D I A Y R K G K T V S C E G Y E S S 120

Qy 121 EDQVYLRGSCGLRYNDYTLTGLOKAKESGKHGPAFSFDYYYKMSADS CNNSGGLTIV 180

Db 121 EDQVYLRGSCGLRYNDYTLTGLOKAKESGKHGPAFSFDYYYKMSADS CNNSGGLTIV 180

QY 181 VLLGLAFVWYKLLPLSDGQISPPPYSEKPPFSRHYQRTNSADPPPGKSKSEFTGQPMNGH 240

Db 181 VLLGLAFVWYKLLPLSDGQISPPPYSEKPPFSRHYQRTNSADPPPGKSKSEFTGQPMNGH 240

Db  
241 GATSGFGSAFTGGGQGYENSGEGFMTGAGTGILGYLFGSNNRAATPFSDSWYPSYPSYP 300

301 GIMNAKISFLEKSSSSSISVCSNSDIAKINIAISGIMNAK 339  
 301 GTWNAAYSPLHGSGSGSYSCNSDITKRTIASGIGTRRR 339

RESULT 7  
US-10-174-590-504  
; Sequence 504, Application US/10174590

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; GENERAL INFORMATION:
;
; APPLICANT: Baker, Kevin P.
;
; APPLICANT: Chen, Jian

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; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.

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; APPLICANT: Smith,Victoria
; APPLICANT: Watanabe,Colin K.
; APPLICANT: Wood,William I.

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; CURRENT FILING DATE: 2002-06-18
; Prior application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 612
; PRO ID: NO. 594

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;
; LENGTH: 339
; TYPE: PRT

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ORGANISM: Homo Sapien  
US-10-174-590-504

Query Match	100.0%;	Score 1879;	DB 14;	Length 339;
Best Local Similarity	100.0%;	Pred. No. 4e-165;		
Matches 339;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0

QY 1 MAAACGPGAGYCLLIGLHLFILTAGPALGMNDDRLMDVKALTLHYRYSRRLDP 60

Db 1 MAAACGPGAGYCLLIGLHLFILTAGPALGMNDDRLMDVKALTLHYRYSRRLDP 60

Qy 6 I P Q L K C V G S T A G C D S Y T P K V I Q C N K G M G Y D V M E C K T D L D I A K F G K T V V S C E G Y E S S 120

Db 61 I P Q L K C V G S T A G C D S Y T P K V I Q C N K G M G Y D V M E C K T D L D I A K F G K T V V S C E G Y E S S 120

Db 121 EDQVYLRGSGCLAEINLDYELGLQKLKESGKQHGPGASFSDFYYXKSSADSCNMSGILITIV 180

Db 181 VLGIAPVYKLFSDGQSPPESEYPPFSHRQRFNTSAGPPPPGKSEFTGQNTGH 240

241 GATGFGSGAFTGGGYYENSGPGFMTGLGTGGIIGLTFGSNRRAATPFSDSWYYPSPSP 300  
 241 GATGFGSGAFTGGGYYENSGPGFMTGLGTGGIIGLTFGSNRRAATPFSDSWYYPSPSP 300  
 241 GATGFGSGAFTGGGYYENSGPGFMTGLGTGGIIGLTFGSNRRAATPFSDSWYYPSPSP 300  
 241 GATGFGSGAFTGGGYYENSGPGFMTGLGTGGIIGLTFGSNRRAATPFSDSWYYPSPSP 300

CY	504	G A N K I S L A S S P S I L C S E D I N A T H G I O U I N K	339
DB	301	G W R A Y S P L H G G S Y S V C S N S D P K I R T A S G Y G T R R	339

RESULT 8  
US-10-176-758-504  
: Sequence 504, Application US/10176758

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; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian

```

; APPLICANT: Goddard, Audrey  
 ; APPLICANT: Godowski, Paul J.  
 ; APPLICANT: Gurney, Austin L.

;  
; APPLICANT: Smith, Victoria  
; APPLICANT: Watanabe, Colin K.  
; APPLICANT: Wood, William I.

; TITLE OF INVENTION: ACIDS ENCODING THE SAME  
 ; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
 ; TITLE OF INVENTION: ACIDS ENCODING THE SAME  
 ; FILE REFERENCE: P3430R1C104  
 ; CIPCLASS AND ICDCLASS: W0606, H01C10/76 769  
 ;

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;
; CURRENT FILING DATE: 2002-06-21
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO: 504

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; LENGTH: 339
; TYPE: PRT
; ORGANISM: Homo Sapien
ITS-10-176-258-504

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Query Match	100.0%	Score 1879	DB 14	Length 339
Best Local Similarity	100.0%	Pred. No. 4e-165		
Matches 339: Conservative	0	Mismatches	0	Indels 0
				Gaps 0

QY 1 MAAACGPGANGYCLILGLHLFLTATGPAIGMNDPDRMLINDVKALTLHYDRYTTSRRLDP 60

Db 1 MAAACGPGANGYCLILGLHLFLTATGPAIGMNDPDRMLINDVKALTLHYDRYTTSRRLDP 60

QY	61	I P O L K C V G G T A G C D S Y T P K V I Q C O N K G M G Y D V M E C K T D L D I A Y F G K T V S C E G Y E S S	120
Db	61	I P O L K C V G G T A G C D S Y T P K V I Q C O N K G M G Y D V M E C K T D L D I A Y F G K T V S C E G Y E S S	120

ORGANISM: Homo Sapiens  
US-10-176-758-504

Query Match	100.0%;	Score 1879;	DB 14;	Length 339;
Best Local Similarity	100.0%;	Pred. No. 4e-165;		
Matches 339; Conservative	0;	Mismatches	0;	Gaps 0

QY	DB
1	1
MAACGPGAGYCLLLGLHLFLTAGPALGWNDDPRMLLDVKALTIHYDRTTSRLDP	MAACGPGAGYCLLLGLHLFLTAGPALGWNDDPRMLLDVKALTIHYDRTTSRLDP
60	60

QY 61 I PQLKCVGGAGACDSTYPRKVIQQCKNGMGSDYDVOMECKTDLDIAAKFGKTVVSCSGYEISS 120

Db 61 I PQLKCVGGAGACDSTYPRKVIQQCKNGMGSDYDVOMECKTDLDIAAKFGKTVVSCSGYEISS 120



PRIOR APPLICATION NUMBER: 60/078886	
PRIOR FILING DATE: 1998-03-20	
PRIOR APPLICATION NUMBER: 60/078939	
PRIOR FILING DATE: 1998-03-20	
PRIOR APPLICATION NUMBER: 60/079664	
PRIOR FILING DATE: 1998-03-27	
PRIOR APPLICATION NUMBER: 60/079786	
PRIOR FILING DATE: 1998-03-27	
PRIOR APPLICATION NUMBER: 60/080107	
PRIOR FILING DATE: 1998-03-31	
PRIOR APPLICATION NUMBER: 60/080194	
PRIOR FILING DATE: 1998-03-31	
PRIOR APPLICATION NUMBER: 60/080327	
PRIOR FILING DATE: 1998-04-01	
PRIOR APPLICATION NUMBER: 60/080333	
PRIOR FILING DATE: 1998-04-01	
PRIOR APPLICATION NUMBER: 60/081049	
PRIOR FILING DATE: 1998-04-08	
PRIOR APPLICATION NUMBER: 60/081070	
PRIOR FILING DATE: 1998-04-08	
PRIOR APPLICATION NUMBER: 60/081195	
PRIOR FILING DATE: 1998-04-09	
PRIOR APPLICATION NUMBER: 60/081838	
PRIOR FILING DATE: 1998-04-15	
PRIOR APPLICATION NUMBER: 60/082568	
PRIOR FILING DATE: 1998-04-21	
PRIOR APPLICATION NUMBER: 60/082569	
PRIOR FILING DATE: 1998-04-21	
PRIOR APPLICATION NUMBER: 60/082704	
PRIOR FILING DATE: 1998-04-22	
PRIOR APPLICATION NUMBER: 60/082797	
PRIOR FILING DATE: 1998-04-22	
PRIOR APPLICATION NUMBER: 60/083322	
PRIOR FILING DATE: 1998-04-28	
PRIOR APPLICATION NUMBER: 60/083495	
PRIOR FILING DATE: 1998-04-29	
PRIOR APPLICATION NUMBER: 60/083496	
PRIOR FILING DATE: 1998-04-29	
PRIOR APPLICATION NUMBER: 60/083499	
PRIOR FILING DATE: 1998-04-29	
PRIOR APPLICATION NUMBER: 60/083559	
PRIOR FILING DATE: 1998-04-29	
PRIOR APPLICATION NUMBER: 60/084366	
PRIOR FILING DATE: 1998-05-05	
PRIOR APPLICATION NUMBER: 60/084414	
PRIOR FILING DATE: 1998-05-06	
PRIOR APPLICATION NUMBER: 60/084639	
PRIOR FILING DATE: 1998-05-07	
PRIOR APPLICATION NUMBER: 60/084640	
PRIOR FILING DATE: 1998-05-07	
PRIOR APPLICATION NUMBER: 60/084643	
PRIOR FILING DATE: 1998-05-07	
PRIOR APPLICATION NUMBER: 60/085573	
PRIOR FILING DATE: 1998-05-15	
PRIOR APPLICATION NUMBER: 60/085579	
PRIOR FILING DATE: 1998-05-15	
PRIOR APPLICATION NUMBER: 60/085580	
PRIOR FILING DATE: 1998-05-15	
PRIOR APPLICATION NUMBER: 60/085582	
PRIOR FILING DATE: 1998-05-15	
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PRIOR FILING DATE: 1998-05-15	
PRIOR APPLICATION NUMBER: 60/086023	
PRIOR FILING DATE: 1998-05-18	
PRIOR APPLICATION NUMBER: 60/086392	
PRIOR FILING DATE: 1998-05-22	
PRIOR APPLICATION NUMBER: 60/086466	
PRIOR FILING DATE: 1998-05-22	
PRIOR APPLICATION NUMBER: 60/087098	
PRIOR FILING DATE: 1998-05-28	
PRIOR APPLICATION NUMBER: 60/087208	
PRIOR FILING DATE: 1998-05-28	
PRIOR APPLICATION NUMBER: 60/087609	

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? PRIOR FILING DATE: 1998-06-02
? PRIOR APPLICATION NUMBER: 60/087759
? PRIOR FILING DATE: 1998-06-02
? PRIOR APPLICATION NUMBER: 60/087827
? PRIOR FILING DATE: 1998-06-03
? PRIOR APPLICATION NUMBER: 60/088025
? PRIOR FILING DATE: 1998-06-04
? PRIOR APPLICATION NUMBER: 60/088028
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? PRIOR APPLICATION NUMBER: 60/089090
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? PRIOR APPLICATION NUMBER: 60/089105
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? PRIOR APPLICATION NUMBER: 60/089514
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? PRIOR APPLICATION NUMBER: 60/089538
? PRIOR FILING DATE: 1998-06-17
? PRIOR APPLICATION NUMBER: 60/089598
? PRIOR FILING DATE: 1998-06-17
? PRIOR APPLICATION NUMBER: 60/089653
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Query Match 100.0%; Score 1879; DB 14; Length 339;
Best Local Similarity 100.0%; Pred. No. 4e-165;
Matches 339; Conservative 0; Mismatches 0; Indels 0; Gaps 0
1 MAAACGPAAGYCCILGILFLTLTGPALGWNDDPRMLLRDKALTLHYDRYTSRLDP 60
Db 1 MAAACGPAAGYCCILGILFLTLTGPALGWNDDPRMLLRDKALTLHYDRYTSRLDP 60
Qy 1POLKCVGATGCDSTYRKVIQCONKMGDGYDVQMECTDLDIAVFGKTVVSCGEYSS 120
Db 61 I POLKCVGATGCDSTYRKVIQCONKMGDGYDVQMECTDLDIAVFGKTVVSCGEYSS 120
Qy 121 EDQVYLRGSCGLEYNLDYTELGLOKLKESGKHGFASFSDDYKKMSADSQMSGLITTV 180

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Db      121 EDQYVLRGSGLEBYNDYTELGLQKLESKGKHGFASPSDYKKMSADSCKNSGLITIV 180
Qy      181 VLLGIADVYVKLFLPSDQYSPPPYSEYPPSHRYQRTNSAGPPPPGFKSEFTGPQNTGH 240
        181 VLLGIADVYVKLFLPSDQYSPPPYSEYPPSHRYQRTNSAGPPPPGFKSEFTGPQNTGH 240
Qy      241 GATSGFSAFTGQGGYENSQSGPFWTGLGTGILLGYLFGSNRAATPFSDSWYTPSPSY 300
        241 GATSGFSAFTGQGGYENSQSGPFWTGLGTGILLGYLFGSNRAATPFSDSWYTPSPSY 300
Db      241 GATSGFSAFTGQGGYENSQSGPFWTGLGTGILLGYLFGSNRAATPFSDSWYTPSPSY 300
Qy      301 GTWNRAYSPLHGGSGSYVCSNSDTKTRTASGYGTRRR 339
        301 GTWNRAYSPLHGGSGSYVCSNSDTKTRTASGYGTRRR 339

```

```

RESULT 11
US-10-176-483-504
; Sequence 504, Application US/10176483
; Publication No. US20030017541A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3430R1C68
; CURRENT FILING DATE: 2002-06-20
; Prior application removed - See file wrapper or Palm
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 504
; LENGTH: 339
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-176-483-504

```

```

Query Match      100.0%; Score 1879; DB 14; Length 339;
Best Local Similarity 100.0%; Pred. No. 4e-165;
Matches 339; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 MAAACGPGAGYCLLGLHLFLTTAGPALGMDPDRMLRDVXALTLHYDRYTSRRLDP 60
        1 MAAACGPGAGYCLLGLHLFLTTAGPALGMDPDRMLRDVXALTLHYDRYTSRRLDP 60
Db      1 MAAACGPGAGYCLLGLHLFLTTAGPALGMDPDRMLRDVXALTLHYDRYTSRRLDP 60
Qy      61 IPOLKCVGAGTACDSTTPKVIQCONKGMGDIYVQMECKTDLDIAYKFGKTVSCGEYSS 120
        61 IPOLKCVGAGTACDSTTPKVIQCONKGMGDIYVQMECKTDLDIAYKFGKTVSCGEYSS 120
Db      61 IPOLKCVGAGTACDSTTPKVIQCONKGMGDIYVQMECKTDLDIAYKFGKTVSCGEYSS 120
Qy      121 EDQYVLRGSGLEBYNDYTELGLQKLESKGKHGFASPSDYKKMSADSCKNSGLITIV 180
        121 EDQYVLRGSGLEBYNDYTELGLQKLESKGKHGFASPSDYKKMSADSCKNSGLITIV 180
Db      121 EDQYVLRGSGLEBYNDYTELGLQKLESKGKHGFASPSDYKKMSADSCKNSGLITIV 180
Qy      181 VLLGIADVYVKLFLPSDQYSPPPYSEYPPSHRYQRTNSAGPPPPGFKSEFTGPQNTGH 240
        181 VLLGIADVYVKLFLPSDQYSPPPYSEYPPSHRYQRTNSAGPPPPGFKSEFTGPQNTGH 240
Db      181 VLLGIADVYVKLFLPSDQYSPPPYSEYPPSHRYQRTNSAGPPPPGFKSEFTGPQNTGH 240
Qy      241 GATSGFSAFTGQGGYENSQSGPFWTGLGTGILLGYLFGSNRAATPFSDSWYTPSPSY 300
        241 GATSGFSAFTGQGGYENSQSGPFWTGLGTGILLGYLFGSNRAATPFSDSWYTPSPSY 300
Db      241 GATSGFSAFTGQGGYENSQSGPFWTGLGTGILLGYLFGSNRAATPFSDSWYTPSPSY 300
Qy      301 GTWNRAYSPLHGGSGSYVCSNSDTKTRTASGYGTRRR 339
        301 GTWNRAYSPLHGGSGSYVCSNSDTKTRTASGYGTRRR 339
Db      301 GTWNRAYSPLHGGSGSYVCSNSDTKTRTASGYGTRRR 339

```

```

RESULT 12
US-10-176-749-504
; Sequence 504, Application US/10176749
; Publication No. US20030017542A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3430R1C76
; CURRENT FILING DATE: 2002-06-20
; Prior application removed - See file wrapper or Palm
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 504
; LENGTH: 339
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-176-749-504

```

```

Query Match      100.0%; Score 1879; DB 14; Length 339;
Best Local Similarity 100.0%; Pred. No. 4e-165;
Matches 339; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 MAAACGPGAGYCLLGLHLFLTTAGPALGMDPDRMLRDVXALTLHYDRYTSRRLDP 60
        1 MAAACGPGAGYCLLGLHLFLTTAGPALGMDPDRMLRDVXALTLHYDRYTSRRLDP 60
Db      1 MAAACGPGAGYCLLGLHLFLTTAGPALGMDPDRMLRDVXALTLHYDRYTSRRLDP 60
Qy      61 IPOLKCVGAGTACDSTTPKVIQCONKGMGDIYVQMECKTDLDIAYKFGKTVSCGEYSS 120
        61 IPOLKCVGAGTACDSTTPKVIQCONKGMGDIYVQMECKTDLDIAYKFGKTVSCGEYSS 120
Db      61 IPOLKCVGAGTACDSTTPKVIQCONKGMGDIYVQMECKTDLDIAYKFGKTVSCGEYSS 120
Qy      121 EDQYVLRGSGLEBYNDYTELGLQKLESKGKHGFASPSDYKKMSADSCKNSGLITIV 180
        121 EDQYVLRGSGLEBYNDYTELGLQKLESKGKHGFASPSDYKKMSADSCKNSGLITIV 180
Db      121 EDQYVLRGSGLEBYNDYTELGLQKLESKGKHGFASPSDYKKMSADSCKNSGLITIV 180
Qy      181 VLLGIADVYVKLFLPSDQYSPPPYSEYPPSHRYQRTNSAGPPPPGFKSEFTGPQNTGH 240
        181 VLLGIADVYVKLFLPSDQYSPPPYSEYPPSHRYQRTNSAGPPPPGFKSEFTGPQNTGH 240
Db      181 VLLGIADVYVKLFLPSDQYSPPPYSEYPPSHRYQRTNSAGPPPPGFKSEFTGPQNTGH 240
Qy      241 GATSGFSAFTGQGGYENSQSGPFWTGLGTGILLGYLFGSNRAATPFSDSWYTPSPSY 300
        241 GATSGFSAFTGQGGYENSQSGPFWTGLGTGILLGYLFGSNRAATPFSDSWYTPSPSY 300
Db      241 GATSGFSAFTGQGGYENSQSGPFWTGLGTGILLGYLFGSNRAATPFSDSWYTPSPSY 300
Qy      301 GTWNRAYSPLHGGSGSYVCSNSDTKTRTASGYGTRRR 339
        301 GTWNRAYSPLHGGSGSYVCSNSDTKTRTASGYGTRRR 339
Db      301 GTWNRAYSPLHGGSGSYVCSNSDTKTRTASGYGTRRR 339

```

```

RESULT 13
US-10-176-914-504
; Sequence 504, Application US/10176914
; Publication No. US20030017543A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.

```

```

; APPLICANT: Zhang,Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3430RIC83
; CURRENT APPLICATION NUMBER: US/10/176,914
; PRIOR APPLICATION DATE: 2002-06-20
; PRIOR APPLICATION removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 504
; LENGTH: 339
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-176-914-504
```

```

Query Match      100.0%; Score 1879; DB 14; Length 339;
Best Local Similarity 100.0%; Pred. No. 4e-165;
Matches 339; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```

QY      1 MAAACGPGAGYCLLIGLHLFLITAGPALGMDPDRMLRDVKALTLHYDRYTSRRLLDP 60
      1 MAAACGPGAGYCLLIGLHLFLITAGPALGMDPDRMLRDVKALTLHYDRYTSRRLLDP 60
DB      1 MAAACGPGAGYCLLIGLHLFLITAGPALGMDPDRMLRDVKALTLHYDRYTSRRLLDP 60
QY      61 IPOLKCVGTAGCDSTTPKVIQCONKGMGDYDVQWECKTDLDIAVYKFTVVSCEGYESS 120
      61 IPOLKCVGTAGCDSTTPKVIQCONKGMGDYDVQWECKTDLDIAVYKFTVVSCEGYESS 120
DB      61 IPOLKCVGTAGCDSTTPKVIQCONKGMGDYDVQWECKTDLDIAVYKFTVVSCEGYESS 120
QY      121 EDQYVLRSGCGLEYNLDYTELGLQKLKESGKHGFASFSDYYKMSADSCKMSGILITIV 180
      121 EDQYVLRSGCGLEYNLDYTELGLQKLKESGKHGFASFSDYYKMSADSCKMSGILITIV 180
DB      121 EDQYVLRSGCGLEYNLDYTELGLQKLKESGKHGFASFSDYYKMSADSCKMSGILITIV 180
QY      181 VLLGIAFVYVKLFLLSDGQVSPPPYSEYPPFSHRQYRFTNSAGPPPGKSEFTGPQNTGH 240
      181 VLLGIAFVYVKLFLLSDGQVSPPPYSEYPPFSHRQYRFTNSAGPPPGKSEFTGPQNTGH 240
DB      181 VLLGIAFVYVKLFLLSDGQVSPPPYSEYPPFSHRQYRFTNSAGPPPGKSEFTGPQNTGH 240
QY      241 GATSGFGSAFTGQOQYENSGPGFWTGLGTGILGYLFGSNRAATPFSDSWYTPSPSYSP 300
      241 GATSGFGSAFTGQOQYENSGPGFWTGLGTGILGYLFGSNRAATPFSDSWYTPSPSYSP 300
DB      241 GATSGFGSAFTGQOQYENSGPGFWTGLGTGILGYLFGSNRAATPFSDSWYTPSPSYSP 300
QY      301 GTWNRAYSPLHGGSGSYVCSNSDTKTRTASGYGTRRR 339
      301 GTWNRAYSPLHGGSGSYVCSNSDTKTRTASGYGTRRR 339
DB      301 GTWNRAYSPLHGGSGSYVCSNSDTKTRTASGYGTRRR 339
```

```

RESULT 14
US-10-176-915-504
; Sequence 504, Application US/10176915
; Publication No. US2003001754A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3430RIC110
; CURRENT APPLICATION NUMBER: US/10/176,915
; CURRENT FILING DATE: 2002-06-21
; PRIOR APPLICATION removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 504
; LENGTH: 339
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-176-915-504
```

```

Query Match      100.0%; Score 1879; DB 14; Length 339;
```

```

Best Local Similarity 100.0%; Pred. No. 4e-165;
Matches 339; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```

QY      1 MAAACGPGAGYCLLIGLHLFLITAGPALGMDPDRMLRDVKALTLHYDRYTSRRLLDP 60
      1 MAAACGPGAGYCLLIGLHLFLITAGPALGMDPDRMLRDVKALTLHYDRYTSRRLLDP 60
DB      1 MAAACGPGAGYCLLIGLHLFLITAGPALGMDPDRMLRDVKALTLHYDRYTSRRLLDP 60
QY      61 IPOLKCVGTAGCDSTTPKVIQCONKGMGDYDVQWECKTDLDIAVYKFTVVSCEGYESS 120
      61 IPOLKCVGTAGCDSTTPKVIQCONKGMGDYDVQWECKTDLDIAVYKFTVVSCEGYESS 120
DB      61 IPOLKCVGTAGCDSTTPKVIQCONKGMGDYDVQWECKTDLDIAVYKFTVVSCEGYESS 120
QY      121 EDQYVLRSGCGLEYNLDYTELGLQKLKESGKHGFASFSDYYKMSADSCKMSGILITIV 180
      121 EDQYVLRSGCGLEYNLDYTELGLQKLKESGKHGFASFSDYYKMSADSCKMSGILITIV 180
DB      121 EDQYVLRSGCGLEYNLDYTELGLQKLKESGKHGFASFSDYYKMSADSCKMSGILITIV 180
QY      181 VLLGIAFVYVKLFLLSDGQVSPPPYSEYPPFSHRQYRFTNSAGPPPGKSEFTGPQNTGH 240
      181 VLLGIAFVYVKLFLLSDGQVSPPPYSEYPPFSHRQYRFTNSAGPPPGKSEFTGPQNTGH 240
DB      181 VLLGIAFVYVKLFLLSDGQVSPPPYSEYPPFSHRQYRFTNSAGPPPGKSEFTGPQNTGH 240
QY      241 GATSGFGSAFTGQOQYENSGPGFWTGLGTGILGYLFGSNRAATPFSDSWYTPSPSYSP 300
      241 GATSGFGSAFTGQOQYENSGPGFWTGLGTGILGYLFGSNRAATPFSDSWYTPSPSYSP 300
DB      241 GATSGFGSAFTGQOQYENSGPGFWTGLGTGILGYLFGSNRAATPFSDSWYTPSPSYSP 300
QY      301 GTWNRAYSPLHGGSGSYVCSNSDTKTRTASGYGTRRR 339
      301 GTWNRAYSPLHGGSGSYVCSNSDTKTRTASGYGTRRR 339
DB      301 GTWNRAYSPLHGGSGSYVCSNSDTKTRTASGYGTRRR 339
```

```

RESULT 15
US-10-173-706-504
; Sequence 504, Application US/10173706
; Publication No. US20030022293A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3430RIC7
; CURRENT APPLICATION NUMBER: US/10/173,706
; CURRENT FILING DATE: 2002-06-17
; PRIOR APPLICATION removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 504
; LENGTH: 339
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-173-706-504
```

```

Query Match      100.0%; Score 1879; DB 14; Length 339;
Best Local Similarity 100.0%; Pred. No. 4e-165;
Matches 339; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```

QY      1 MAAACGPGAGYCLLIGLHLFLITAGPALGMDPDRMLRDVKALTLHYDRYTSRRLLDP 60
      1 MAAACGPGAGYCLLIGLHLFLITAGPALGMDPDRMLRDVKALTLHYDRYTSRRLLDP 60
DB      1 MAAACGPGAGYCLLIGLHLFLITAGPALGMDPDRMLRDVKALTLHYDRYTSRRLLDP 60
QY      61 IPOLKCVGTAGCDSTTPKVIQCONKGMGDYDVQWECKTDLDIAVYKFTVVSCEGYESS 120
      61 IPOLKCVGTAGCDSTTPKVIQCONKGMGDYDVQWECKTDLDIAVYKFTVVSCEGYESS 120
DB      61 IPOLKCVGTAGCDSTTPKVIQCONKGMGDYDVQWECKTDLDIAVYKFTVVSCEGYESS 120
QY      121 EDQYVLRSGCGLEYNLDYTELGLQKLKESGKHGFASFSDYYKMSADSCKMSGILITIV 180
      121 EDQYVLRSGCGLEYNLDYTELGLQKLKESGKHGFASFSDYYKMSADSCKMSGILITIV 180
DB      121 EDQYVLRSGCGLEYNLDYTELGLQKLKESGKHGFASFSDYYKMSADSCKMSGILITIV 180
```

Qy	181	VLLGIATVWVYKLF	PLSDCOYSP	PPYSEYPP	PSHR	YORFTNSAG	PPPGKSEFTG	PONTGH	240
Db	181	VLLGIATVWVYKLF	PLSDCOYSP	PPYSEYPP	PSHR	YORFTNSAG	PPPGKSEFTG	PONTGH	240
Qy	241	GATSGFGSAFTG	QGGYENSG	PGFWTGL	GTGII	GYLFGSNRAAT	PFSDSWY	PPSY	300
Db	241	GATSGFGSAFTG	QGGYENSG	PGFWTGL	GTGII	GYLFGSNRAAT	PFSDSWY	PPSY	300
Qy	301	GTWNRAYSPLH	GSGSYVC	SNSDTK	TRTASG	YGT	RRR		339
Db	301	GTWNRAYSPLH	GSGSYVC	SNSDTK	TRTASG	YGT	RRR		339

Search completed: July 14, 2005, 20:37:49  
 Job time : 107.864 secs

*This Page Blank (uspto)*



GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: July 14, 2005, 20:14:28 ; Search time 23.2757 Seconds

(without alignments)  
1401.351 Million cell updates/sec

Title: US-10-019-151C-2

Perfect score: 1879  
Sequence: 1 MAACGPGAGYCTLLGLHL.....CNSDPTKTRTASGSGTRRR 339

Scoring table:

BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 9621673 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR 79: \*  
1: p1r1: \*  
2: p1r2: \*  
3: p1r3: \*  
4: p1r4: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	499.5	26.6	323	2 T24582	hypothetical prote
2	115	6.1	407	2 T21956	hypothetical prote
3	115	6.1	1400	2 T31555	hypothetical prote
4	113	6.0	2090	2 S26058	probable transform
5	108.5	5.8	528	2 G02127	fus-like protein -
6	107	5.7	532	2 S27372	beta-fructofuranos
7	106.5	5.7	748	2 T04011	hypothetical prote
8	106	5.6	455	1 T21089	acid phosphatase (
9	106	5.6	1585	2 T31611	hypothetical prote
10	105	5.6	3300	2 D70575	probable PP2 prote
11	104	5.5	353	2 B34504	heterogeneous nucl
12	103.5	5.5	373	2 S40777	heterogeneous ribo
13	102.5	5.5	342	2 T45886	RNA-binding protei
14	101.5	5.4	794	2 T10519	pre-pro-1egumlin -
15	101.5	5.4	1844	2 T51890	related to Nup98-N
16	100.5	5.3	186	2 S28021	rab18 protein - Ar
17	100.5	5.3	314	2 T08675	hypothetical prote
18	100.5	5.3	462	4 S33798	FUS/CHOP mutant fu
19	100.5	5.3	526	1 S33799	RNA-binding protei
20	100	5.3	615	2 T29550	hypothetical prote
21	99.5	5.3	365	2 A34840	heterogeneous ribo
22	99.5	5.3	419	2 T04886	DAG protein homolo
23	99	5.3	632	2 T02627	hypothetical prote
24	98.5	5.2	320	1 DDX1	helix-destabilizin
25	98.5	5.2	320	1 A44485	heterogeneous ribo
26	98.5	5.2	330	2 S04617	heterogeneous ribo
27	98	5.2	1436	2 B70520	probable PP2 prote
28	98	5.2	1567	2 S11672	ice nucleation pro
29	97.5	5.2	925	2 J02033	G protein-coupled

30	96.5	5.1	320	2 S30192	heterogeneous ribo
31	96.5	5.1	320	2 S02061	heterogeneous ribo
32	96.5	5.1	404	2 B84745	probable RNA-bindi
33	96.5	5.1	925	2 T19361	hypothetical prote
34	96.5	5.1	1732	2 T43026	probable DNA-direc
35	96	5.1	159	2 C49723	ecdysone-dependent
36	95.5	5.1	334	2 S53490	RNA-binding protei
37	95.5	5.1	658	2 T08153	cysteine proteinas
38	95	5.1	532	2 S27373	beta-fructofuranos
39	95	5.1	671	2 A35912	homeotic protein o
40	95	5.1	1239	2 T13809	homeotic protein o
41	94.5	5.0	284	2 B41224	homeotic protein p
42	94.5	5.0	298	2 A40616	34K antigen - Myco
43	94.5	5.0	406	2 G71404	probable ribonucle
44	94.5	5.0	465	2 S33680	ribonucleoprotein
45	94.5	5.0	471	2 S33679	ribonucleoprotein

#### ALIGNMENTS

##### RESULT 1

T24582

hypothetical protein T06D8.9 - Caenorhabditis elegans

C/Species: Caenorhabditis elegans

C/Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #ext\_change 09-Jul-2004

C/Accession: T24582

R/Palmer, S.

submitted to the EMBL Data Library, April 1995

A/Reference number: Z19909

A/Accession: T24582

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: DNA

A/Residues: 1-323 <WIL>

A/Cross-references: UNIPROT:Q22254; EMBL:Z49130; PIDR:CAAB8972.1; GSPDB:GN00020; CESP:T

A/Experimental source: clone T06D8

C/Genetics:

A/Gene: CESP:T06D8.9

A/Map position: 2

A/Intons: 7/3; 33/1; 109/3; 239/2

Query Match	Score	26.6%	DB 2	Length	323;
Best Local Similarity	34.8%	Pred. No. 1.3e-31;			
Matches	120;	Conservative	40;	Mismatches	88;
				Indels	97;
				Gaps	9;
QY	35	DRMLADVYALTLHRYDRTYSRLDPI	PQLKCVGAGCDSYTPKVIQCONKMGSDYDQ	94	
Db	36	DKVLADVSAITLHKIGKMTTGRVSP	PTQLKCVGSAK-GAFTPKVVCANQGFDSYDQ	94	
QY	95	WECRTDLDIAVYFKGKTIVSGEYSE	EDQVLRGSGLEINMDYBL-GLQKLKESGKH	153	
Db	95	WRCDDADLPDMDFGSISSCEGYDA	EDPYIRGSGLEYRELYNSASGNRSVRSKSD	154	
QY	154	GFASFSDYVYKWSADSCMSGLITV	VLGIAFVYKFLPSDQ-----	198	
Db	155	RNDQFA-----	TFVVAFATYIYIAWNTNNQNPSSG	YTSGGSGP	196
QY	199	YSPPYSEVYPPFSHRQRTNSAGPP	PFKSEFT---GPQNTG	239	
Db	197	GGGSGGGGGGPGYPSAPFPYDY	-----SKPPYGRGDSGSGGCGSS	243	
QY	240	HGATSGFGSAFTGQCCQYENSQPG	FTGLTGILGLTFPS-----NRATP	PSDSMYTR	294
Db	244	SGGASGSGA-----	NNGGSFTWGAIGIAGTILASS	PLNNNAVYRP-----	285
QY	295	YPPSYGTWNRAYSPLHGSGSYVCS	NEDYTRTASGYGTRRR	339	
Db	286	-----RYNKGFPQDTGRFSSDS	SSSPSTSMRSSSGYGGITRR	323	

##### RESULT 2

T21956

hypothetical protein F38B7.3 - Caenorhabditis elegans



Db 182 GCG 184

# RESULT 6

S27372

beta-fructofuranosidase (EC 3.2.1.26) 1 precursor - yeast (*Saccharomyces cerevisiae*)

N/Alternate names: invertase; saccharase

C/Species: *Saccharomyces cerevisiae*

C/Date: 23-Apr-1993 #sequence\_revision 23-Apr-1993 #text\_change 09-Jul-2004

C/Accession: S27372, S25441

R/Hohmann, S.

submitted to the EMBL Data Library, November 1988

A/Reference number: S27372

A/Accession: S27372

A/Molecule type: DNA

A/Residues: 1-532 <HOH>

A/Cross-references: UNIPROT:P10594, EMBL:X07570, NID:g4567, PIDN:CAA30457.1, PID:g4568

R/Hohmann, S.; Gozalbo, D.

Mol. Gen. Genet. 211, 446-454, 1988

A/Title: Structural analysis of the 5' regions of yeast SUC genes revealed analogous pal

A/Reference number: S25439, MUID:88216256, PMID:2835632

A/Accession: S25441

A/Molecule type: DNA

A/Residues: 1-74 <HO2>

A/Cross-references: EMBL:X07570

C/Genetic81

A/Map position: 7R

C/Superfamily: beta-fructofuranosidase

C/Keywords: glycosidase; hydrolase

F/1-19/Domain: signal sequence #status predicted <SIG>

F/20-532/Product: beta-fructofuranosidase 1 #status predicted <MAT>

Query Match 5.7%; Score 107; DB 2; Length 532;

Best Local Similarity 24.1%; Pred. No. 1.1;

Matches 92; Conservative 40; Mismatches 144; Indels 106; Gaps 24;

14 LLLGLHFLTAG-----PALGM-NDPRLMLRDVRLTLH-Y 49

1 MLQAFPLFL-AGFAKISAMTNETSDRLVHFTPKKGMWMDNG-LWYDAKKGXWMLY 58

50 DRYTTSRLDPIPOLKCVGAGCDSTY-----PKVIQCCNKMGDGYDVMECTTDIDIA 104

59 FQYNPN--DTWGLPLFWGHATSDDLTHMODEFVALPAKKKSGAV-----SGSNVID 109

105 YK-----FGKTV-----VSCGEYS--SEDOYVLKSGGLEYNLD--YTETGLQK--L 146

110 YNNTSGFNFNTIDPRQCAVIMTYNTPESEROY-----SYLDDGYFTETQKRPVL 162

147 KESGKHGFASPSDYT---KSSADSCKMSGLITVLLGI-AFVVYKLFSLDG--- 197

163 AANSTQ--FRDPKFWYBPSKWMIMTAKSQDYKIRIYSSDDLKSMKLESFANEGFLGY 220

198 QYSP-----PYSEYPPFSHRVQFTNSAGPPRG-FKSEPTGQNTGH-----GATS 244

221 QYBPGILBYPSBDDPKSHVMWFTISNPGAPAGSGSNQYVSGFNGHHPAEPDNGSRV 280

245 GFGSAPFGQGYKNSGPFMTGLTGILGTFGSNRAATPFSDSWYTPSPSPSGTWN 304

281 DFGMDYVALQTFPTDPTY-----GSAIGIAMSNN-----WYSNAPVBNP--WR 323

305 RAYSPPLHGGSGSYVCSNSTDK 326

324 SMSLVLPFSLNTEYQANPETE 345

Db

Qy

Db

Qy

Db

Qy

Db

Qy

Db

Qy

Db

Qy

Db

Qy

Db

Qy

Db

Qy

Db

Qy

Db

Qy

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Qy

Db

Qy

R/Beyan, M.; Murphy, G.; Ridley, P.; Hudson, S.; Bancroft, I.; Mewes, H.W.; Mayer, K.F.

submitted to the Protein Sequence Database, March 1999

A/Reference number: Z15184

A/Accession: T04011

A/Molecule type: DNA

A/Residues: 1-748 <BEV>

A/Cross-references: UNIPROT:Q9T0G5, EMBL:AL049481

C/Experimental source: cultivar Columbia; BAC clone T5L19

C/Genetic81

A/Map position: 4

A/Introns: 67/2; 209/3; 271/3; 305/3; 329/3; 367/3; 691/1

A/Note: T5L19.200

Query Match 5.7%; Score 106.5; DB 2; Length 748;

Best Local Similarity 24.7%; Pred. No. 1.7;

Matches 41; Conservative 23; Mismatches 45; Indels 57; Gaps 10;

195 SDGQSPSPSEYPP--PFSHRVQFTNSAG-----PPPCPKSE-----FTGPON 237

396 SRGPHAHPIYDHPRGYSQ-GSYNPSRFGGYPPQAHMPRGYGTDMORPPYSGPN 454

238 TGHGATSGFSAFTGQGYENSGP-----GFWTGLGTG---ILGYLFGSNRA-----A 283

455 -----YGRGQASAGVPVPPSGPVPSPAPGPPPLSGVSYGQSGHGPXYGHA 502

284 TPSPDSNY-----YPSYPSYPPGTRNARYPLGSGSY 317

503 APYSQNGYQQTGYGTYPKPYDSNPMQP-PYGGSYPPAGGQSGY 547

Db

Qy

Db

Qy

Db

Qy

Db

Qy

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Qy

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Qy

Oy	240	HGATSGGSAFGGQOQYE-NSGCGFMTGATGSLGLYLF-----	277
	209	H-----NDNGYSPFDLGGVHHVAGST-ETYGYYIYEGMDPWNTQYDMLKRDLTIA	25
Oy	278	GSNRATPPSDSMYF-SYPPSPFGIMTNA	306
Db	258	NSNRRAHP---WIFFGHRPFYCSNVNA	283

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RESULT 9
T31611
hypochemical protein Y50B8A.g - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999
C:Accession: T31611
R:Steward, C.
submitted to the EMBL Data Library, September 1999
A:Reference number: Z21047
A:Accession: T31611
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-1585 <ML>
A:Cross-references: EMBL:AL117200; NID:e1549770; PIND:CBMS5050.1; CESP:Y50B8A.g
A:Experimental source: clone Y50B8A
C:Genetic8
A:Gene: CESP:Y50B8A.g
A:introns: 25/3; 60/1; 133/2; 217/3; 270/3; 337/2; 400/1; 746/2

```

RESULT 10  
D70575  
probable ppe protein - Mycobacterium tuberculosis (strain H37Rv)  
C:Species: Mycobacterium tuberculosis  
C:date: 17-Jul-1998 #sequence\_revision 17-Jul-1998 #text\_change 22-Oct-1999  
C:Accession: D70575  
R:Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, R.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.; Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.  
Nature 393, 537-544, 1998  
A:Authors: Squares, R., Salston, J.E., Taylor, K., Whitehead, S., Barrell, B.G.  
A:title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome  
A:Reference number: A70500; MUID:98295987; PMID:9634230  
A:Accession: D70575  
A:Status: preliminary; nucleic acid sequence not shown; translation not shown  
A:Molecule type: DNA  
A:Residues: 1-3300 <COO>  
A:Cross-references: GB:D25324; GB:AL123456; NID:g3261760; PIDN:CAB08587.1; PID:e1299834;  
A:Experimental source: Strain H37Rv  
C:Genetics:  
C:Gene: ppe

Query Match 5.6%; Score 105; DB 2; Length 3300;  
 Best Local Similarity 38.0%; Pred. No. 13;  
 Matches 30; Conservative 8; Mismatches 15; Indels 26; Gaps 6

218 TNSAG-----PPPPGFKSEPTGPQ---NTGHGATSGRGSAPFTGGQGIYENSQPRW 264

Db 2303 TSGAGPVVILPLDIPPAFGFQGNSTTGPSSGFNFNSGCTSSSSGFQNV-----GANN--GFW 2355  
 QY 265 ----TGLGTGAILGLYFGS 279  
 Db 2356 NTAPAGIGNSGLQ--FGS 2372

RESULT 11

B34504  
heterogeneous nuclear ribonucleoprotein B1 - human  
N/Alternate names: heterogeneous nuclear ribonuclear particle protein B1; hnRNP protein B1; NEPR  
N/Contains: heterogeneous nuclear ribonucleoprotein A2  
C/Species: Homo sapiens (man)  
C/Date: 22-Jun-1990 #sequence revision 22-Jun-1990 #text change 09-Jul-2004  
C/Accession: A56845; B34504; A34504; S48057; PC2222; E61013; B56845  
R/Kozu, T.; Henrich, B.; Schaefer, K.P.  
Genomic 25, 365-371, 1995  
A/Title: Structure and expression of the gene (HNRPA2B1) encoding the human hnRNP protein  
A/Reference number: A56845; MUID:95309902; PMID:7789369  
A/Accession: A56845  
A/Status: nucleic acid sequence not shown  
A/Molecule type: DNA  
A/Residues: 1-353 <KOZ>  
A/Cross-references: UNIPROT:P22626; GB:D28877; NID:G55642; PIDN:BA06031.1; PID:G55643  
R/Burd, C.G.; Swanson, M.S.; Goerlach, M.; Dreyfuss, G.  
Proc. Natl. Acad. Sci. U.S.A. 86, 9788-9792, 1989  
A/Title: Primary structures of the heterogeneous nuclear ribonucleoprotein A2, B1, and  
A/Reference number: A34504; MUID:90093350; PMID:2557628  
A/Accession: B34504  
A/Status: preliminary  
A/Molecule type: mRNA  
A/Residues: 1-353 <BUR>  
A/Cross-references: GB:M29064; NID:G337452; PIDN:AA60271.1; PID:G337453  
A/Accession: A34504  
A/Status: preliminary  
A/Molecule type: mRNA  
A/Residues: 1-2,15-353 <BU2>  
A/Cross-references: GB:M29064  
R/Diamond, J.; Ruggiu, M.; Saccone, S.; della Valle, G.; Riva, S.  
Nucleic Acids Res. 22, 1995-2002, 1994  
A/Title: Two homologous genes, originated by duplication, encode the human hnRNP protein  
A/Reference number: S48057; MUID:94301779; PMID:8029005  
A/Accession: S48057  
A/Status: preliminary  
A/Molecule type: DNA  
A/Residues: 1-353 <BIA>  
A/Cross-references: EMBL:U09122  
R/Prasad, S.; Walent, J.; Dittschilo, A.  
Biochem. Biophys. Res. Commun. 204, 772-779, 1994  
A/Title: ADP-ribosylation of heterogeneous ribonucleoproteins in HeLa cells.  
A/Reference number: PC2221; MUID:95071393; PMID:7980541  
A/Accession: PC2222  
A/Molecule type: Protein  
A/Residues: 'XXX', '83-86', 'X', '88-93', 'X', '95-100' <PRA>  
A/Experimental source: HeLa cells  
R/Note: This protein was shown to be ADP-ribosylated  
R/Bau, G.; Rasmussen, H.H.; Van Den Bulcke, M.; Van Damme, J.; Puype, M.; Geiser, B.;  
Electrophoresis 11, 528-536, 1990  
A/Title: Two-dimensional gel electrophoresis, protein electrophoresis and microsequencing  
A/Reference number: A61002; MUID:91031404; PMID:1699755  
A/Accession: E61013  
A/Molecule type: Protein  
A/Residues: 63-69;204-212;214-220, 'F', 221-228 <BAV>  
C/Genetic8:  
A/Gene: GDB:HNRPA2B1  
A/Cross-references: GDB:377778; OMIM:600124  
A/Map position: 7p15-7p15  
A/Intons: 2/3; 14/3; 100/3; 171/1; 205/1; 232/1; 253/1; 293/1; 334/1  
C/Superfamily: helix-stabilizing protein; ribonucleoprotein repeat homology  
C/Keywords: alternative splicing; duplication; nucleus; RNA binding  
C/1-2,15-353/Domain: heterogeneous ribonuclear particle protein A2 <HA2>  
C/23-88/Domain: ribonucleoprotein repeat homology <RNM1>



QY 311 HGGSGSYVCNSDPTKRTA--SGYGGR 337  
 Db 425 GGGSGSYPCGGGIEGOTGTGTFPGSGGSR 453

## RESULT 15

TS1890  
 related to Nup98-Nup96 precursor [imported] - Neurospora crassa  
 N/Alternate names: Protein B23111.20  
 C/Species: Neurospora crassa  
 C/Date: 20-Oct-2000 #sequence\_revision 20-Oct-2000 #text\_change 20-Oct-2000  
 C/Accession: TS1890  
 R/Schulte, U.; Aign, V.; Hoheisel, J.; Brandt, P.; Partmann, B.; Holland, R.; Nyakatura,  
 submitted to the Protein Sequence Database, August 2000  
 A/Reference number: Z25858  
 A/Accession: TS1890  
 A/Status: preliminary  
 A/Molecule type: DNA  
 A/Residues: 1-1844 <SCH>  
 A/Cross-references: EMBL:AL391572; GSPDB:GN00116; NCSP:B23111.20  
 A/Experimental source: BAC clone B23111; strain OR74A  
 C/Genetics:  
 A/Gene: NCSP:B23111.20  
 A/Map position: 6  
 A/Introns: 34/1; 1281/3

Query Match 5.4%; Score 101; DB 2; Length 1844;  
 Best Local Similarity 35.0%; Pred. No. 13;

Matches 48; Conservative 8; Mismatches 51; Indels 30; Gaps 9;

QY 215 QRFNAGPPPPGFKSBFTGPONTGHG-ATSGFGS-AFTGQOG-----YENSGPGFW 264  
 Db 11 QNTMTSGGRSSSGFTN-TCTTGTFGAATGFGAPAGTCTTGGLFGSGTTGTTGGFG 69  
 QY 265 T---GIATGILGY--LFGSNRAATPFSDSWYTPSPYPTGTNRRAYSPLHGSGSYS 318  
 Db 70 TWTAGGFGTGGGFGAKPAFGSTPATY---GGGLFGSSTATATGT-----GGFGSTG 117  
 QY 319 VCSNPTKTRTASGYCG 335  
 Db 118 FGSNTAT-TGTGFGSG 133

Search completed: July 14, 2005, 20:33:16  
 Job time : 31.2757 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

# OM protein - protein search, using sw model

Run on: July 14, 2005, 19:55:46 ; Search time 106.243 Seconds  
(without alignments)  
1633.949 Million cell updates/sec

Title: US-10-019-151C-2

Sequence: 1 MAAACGGAAAGCCTGAGLH.....CSNSDTRRTASGVTGTRRR 339

Scoring table: BIOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : UnIProt 03.\*  
1: uniprot\_sprot.\*  
2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1879	100.0	339	2	Q96BY9
2	1867	99.4	339	2	Q96BY9
3	1676	89.2	303	2	Q9UN23
4	1428	76.0	363	2	Q8R300
5	1427	75.9	334	2	Q8C6G7
6	1427	75.9	363	2	Q8D8R1
7	1418	75.5	363	2	Q8R233
8	1387	73.8	334	2	Q6A1X2
9	1176.5	62.6	292	2	Q8C2E1
10	499.5	26.6	323	2	Q22254
11	361.5	19.2	357	2	Q7S303
12	124	6.6	966	2	Q7RW88
13	124	6.6	966	2	Q01385
14	124	6.6	977	2	Q8X005
15	122	6.5	974	2	Q9UVL3
16	121.5	6.5	421	2	Q6Z8B6
17	121	6.4	587	2	Q98SL7
18	117	6.2	954	2	Q6C1L8
19	116.5	6.2	963	2	Q9UVT2
20	115	6.1	407	2	Q20151
21	115	6.1	942	2	Q9W4N4
22	113.5	6.0	555	2	Q62D57
23	113	6.0	410	2	Q7ZUR3
24	113	6.0	2090	1	N214 HUMAN
25	113	6.0	2091	1	Q7SR47
26	113	6.0	2119	2	Q86XJ3
27	112.5	6.0	197	2	Q9ATK3
28	112.5	6.0	366	2	Q8WYF8
29	112	6.0	1519	2	Q7Z3C4
30	111	5.9	571	2	Q7UR98
31	111	5.9	2850	1	HORN_HUMAN

32	110.5	5.9	592	2	Q98SL6	Q98SL6
33	110.5	5.9	2058	2	Q7PUR9	Q7PUR9
34	110	5.9	350	2	Q8C2H8	Q8C2H8
35	110	5.9	898	2	Q8K588	Q8K588
36	110	5.9	911	1	ILP3 MOUSE	Q92144
37	110	5.9	911	1	Q812A1	Q812A1
38	109.5	5.8	399	2	Q7ZXJ3	Q7ZXJ3
39	109	5.8	410	2	Q16388	Q16388
40	109	5.8	633	2	Q86AP6	Q86AP6
41	108.5	5.8	528	2	Q13344	Q13344
42	108	5.7	262	2	Q90X89	Q90X89
43	107.5	5.7	360	2	Q9LK74	Q9LK74
44	107.5	5.7	365	2	Q61P29	Q61P29
45	107.5	5.7	469	2	Q6WNS8	Q6WNS8

## ALIGNMENTS

RESULT 1  
Q96BY9 PRELIMINARY; PRT; 339 AA.  
ID Q96BY9  
AC Q96BY9  
DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)  
DE Hypothetical protein MG8721 (FOAP-7) (AAC1367).  
GN Name=MG8721; Synonym=foap-7; ORFName=UHQ1967;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Uterus;  
RX MEDLINE=23388257; PubMed=12477932; DOI=10.1073/pnas.242603699;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hultey S.W.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Saplenton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Ustin T.B., Tsohynki S., Carninci P., Prange C.,  
RA Raha S.S., Loughellano N.A., Peters G.J., Abramson R.D., Mulhally S.J.,  
RA Bobak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hultey S.W.,  
RA Villalón D.R., Muzny D.M., Sodergren R.J., Lu X., Gibbs R.A.,  
RA Pabey J., Helton B., Ketterman M., Madan A., Rodriguez S., Sanchez A.,  
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
RA Krzyzanski M.I., Skalkida U., Smallus D.E., Schnerch A., Schein J.E.,  
RA Jones S.J., Marra M.A.,  
RT "Generation and initial analysis of more than 15,000 full-length human  
and mouse cDNA sequences.";  
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
[2]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Uterus;  
RX Strausberg R.;  
RA Submitted (Oct-2001) to the EMBL/GenBank/DBJ databases.  
RN [3]  
RP SEQUENCE FROM N.A.  
RC Fujii Y., Tsuritani K., Yajima Y., Amemiya T., Uka Y., Naito K.,  
RA Kawaguchi A., Takayama K.;  
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.  
[4]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=22887296; PubMed=12975309; DOI=10.1101/gr.1293003;  
RA Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D., Brush J.,  
RA Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,  
RA Baton D., Foster J., Grimaldi C., Gu O., Hase P.E., Heidens S.,  
RA Huang A., Kim H.S., Klimoweki L., Jin Y., Johnson S., Lee J.,



RA Lewis L., Liao D., Mark M., Robbie E., Sanchez C., Schoenfeld J.,  
RA Seshagiri S., Simmons L., Singh V., Smith V., Stinson J., Vagstad A.,  
RA Vandlen R., Watanabe C., Wiesend D., Woods K., Xie M.H., Yantura D.,  
RA Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I.,  
RA Godowski P.,  
RT "The secreted protein discovery initiative (SPDI), a large-scale  
RT effort to identify novel human secreted and transmembrane proteins: a  
RT bioinformatics assessment.";  
RL Genome Res. 13:2265-2270(2003).  
DR EMBL; BC015012; AAI15012.1; -;  
DR EMBL; AB028926; BAB2465.1; -;  
DR EMBL; AY359104; AAQ89462.1; -;  
DR InterPro; IPR009567; DUF1183.  
DR Pfam; PF06682; DUF1183; 1.  
KM Hypothetical protein.  
SQ SEQUENCE 339 AA; 36975 MW; 83CC0517AB635FE9 CRC64;  
  
Query Match 100.0%; Score 1879; DB 2; Length 339;  
Best Local Similarity 100.0%; Pred. No. 9e-135;  
Matches 339; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 MAACGPGAGYCLLGLHLFLITAGPALGMDPRMLRDVYKALTLHYDRYTSRRLD 60  
DB 1 MAACGPGAGYCLLGLHLFLITAGPALGMDPRMLRDVYKALTLHYDRYTSRRLD 60  
QY 61 IPOLKCVGTAGCDSTTPKVIQCONKGMGVYVQWCKTDLDIAVYKGVTSCEGYSS 120  
DB 61 IPOLKCVGTAGCDSTTPKVIQCONKGMGVYVQWCKTDLDIAVYKGVTSCEGYSS 120  
QY 121 EDQYVLRSGCGLEYNLDYTELGLOKLKESGKHGFASFDYKKMSADSCKMSGLITIV 180  
DB 121 EDQYVLRSGCGLEYNLDYTELGLOKLKESGKHGFASFDYKKMSADSCKMSGLITIV 180  
QY 121 VILGIAFVYVKFLPSDQYSPPPYSBPPFSHRYPFTNSAGPPPGFKSBFTGPQNTGH 240  
DB 121 VILGIAFVYVKFLPSDQYSPPPYSBPPFSHRYPFTNSAGPPPGFKSBFTGPQNTGH 240  
QY 181 VILGIAFVYVKFLPSDQYSPPPYSBPPFSHRYPFTNSAGPPPGFKSBFTGPQNTGH 240  
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QY 241 GATSGGSAFTQOQGYENSPPGFWTGLGTGILGYLFGSNRAATPPSDSWYPSYSP 300  
DB 241 GATSGGSAFTQOQGYENSPPGFWTGLGTGILGYLFGSNRAATPPSDSWYPSYSP 300  
QY 301 GTWNRAYSPLHGGSGSYVCSNSDTKTRTASGYGTRRR 339  
DB 301 GTWNRAYSPLHGGSGSYVCSNSDTKTRTASGYGTRRR 339  
  
RESULT 2  
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AC QY683;  
DT 01-NOV-1999 (T-EMBLrel. 12, Created)  
DT 01-NOV-1999 (T-EMBLrel. 12, Last sequence update)  
DT 05-JUL-2004 (T-EMBLrel. 27, Last annotation update)  
DE HSPC035 protein (XTP3).  
GN Name=XTP3;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=20499367; PubMed=11042152; DOI=10.1101/gr.140200;  
RA Zhang Q.H., Ye M., Wu X.Y., Ren S.X., Zhao M., Zhao C.J., Fu G.,  
RA Shen Y., Fan H.Y., Lu G., Zhong M., Xu X.R., Han Z.G., Zhang J.W.,  
RA Tao J., Huang Q.H., Zhou J., Hu G.X., Gu J., Chen S.J., Chen Z.,  
RT "Cloning and functional analysis of CDNA with open reading frames for  
RT 300 previously undefined genes expressed in CD34+ hematopoietic  
RT stem/progenitor cells.";  
RL Genome Res. 10:1546-1560(2000).  
RN [2]  
RP SEQUENCE FROM N.A.  
RA Liu Y., Cheng J., Lu Y., Wang G., Zhang L., Chen J., Li L.,  
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.

DR EMBL; AF100748; AAD43012.1; -;  
DR EMBL; AF490252; AAO85460.1; -;  
DR InterPro; IPR009567; DUF1183.  
DR Pfam; PF06682; DUF1183; 1.  
SQ SEQUENCE 339 AA; 36979 MW; FB6FD94B3879FAA8 CRC64;  
  
Query Match 99.4%; Score 1867; DB 2; Length 339;  
Best Local Similarity 99.4%; Pred. No. 7.4e-134;  
Matches 337; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
  
QY 1 MAACGPGAGYCLLGLHLFLITAGPALGMDPRMLRDVYKALTLHYDRYTSRRLD 60  
DB 1 MAACGPGAGYCLLGLHLFLITAGPALGMDPRMLRDVYKALTLHYDRYTSRRLD 60  
QY 61 IPOLKCVGTAGCDSTTPKVIQCONKGMGVYVQWCKTDLDIAVYKGVTSCEGYSS 120  
DB 61 IPOLKCVGTAGCDSTTPKVIQCONKGMGVYVQWCKTDLDIAVYKGVTSCEGYSS 120  
QY 121 EDQYVLRSGCGLEYNLDYTELGLOKLKESGKHGFASFDYKKMSADSCKMSGLITIV 180  
DB 121 EDQYVLRSGCGLEYNLDYTELGLOKLKESGKHGFASFDYKKMSADSCKMSGLITIV 180  
QY 121 VILGIAFVYVKFLPSDQYSPPPYSBPPFSHRYPFTNSAGPPPGFKSBFTGPQNTGH 240  
DB 121 VILGIAFVYVKFLPSDQYSPPPYSBPPFSHRYPFTNSAGPPPGFKSBFTGPQNTGH 240  
QY 181 VILGIAFVYVKFLPSDQYSPPPYSBPPFSHRYPFTNSAGPPPGFKSBFTGPQNTGH 240  
DB 181 VILGIAFVYVKFLPSDQYSPPPYSBPPFSHRYPFTNSAGPPPGFKSBFTGPQNTGH 240  
QY 241 GATSGGSAFTQOQGYENSPPGFWTGLGTGILGYLFGSNRAATPPSDSWYPSYSP 300  
DB 241 GATSGGSAFTQOQGYENSPPGFWTGLGTGILGYLFGSNRAATPPSDSWYPSYSP 300  
QY 301 GTWNRAYSPLHGGSGSYVCSNSDTKTRTASGYGTRRR 339  
DB 301 GTWNRAYSPLHGGSGSYVCSNSDTKTRTASGYGTRRR 339  
  
RESULT 3  
QYUN23 PRELIMINARY; PRT; 303 AA.  
AC QYUN23;  
DT 01-MAY-2000 (T-EMBLrel. 13, Created)  
DT 01-MAY-2000 (T-EMBLrel. 13, Last sequence update)  
DT 01-MAR-2004 (T-EMBLrel. 26, Last annotation update)  
DE NP0003.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Normal pituitary;  
RA Huang Q., Zhou J., Song H., Peng J., Zhang Q., Fu G., Dai M., Mao Y.,  
RA Mao M., Chen Z., Chen J.,  
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.  
RN [2]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Normal pituitary;  
RA Hu R.;  
RL Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF078855; AAD44487.1; -;  
DR InterPro; IPR009567; DUF1183.  
DR Pfam; PF06682; DUF1183; 1.  
SQ SEQUENCE 303 AA; 33338 MW; 771609A6CF690F07 CRC64;  
  
Query Match 89.2%; Score 1676; DB 2; Length 303;  
Best Local Similarity 99.7%; Pred. No. 2.2e-119;  
Matches 302; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
  
QY 37 MLRDVYKALTLHYDRYTSRRLDPIPOLKCVGTAGCDSTTPKVIQCONKGMGVYVQW 96  
DB 1 MLRDVYKALTLHYDRYTSRRLDPIPOLKCVGTAGCDSTTPKVIQCONKGMGVYVQW 96  
QY 97 CKTDLDIAVYKGVTSCEGYSSDQYVLRSGCGLEYNLDYTELGLOKLKESGKHGF 156



Db 61 CKTDLDIAVKEKTVSCGEGYSSSDQVYLRGSCGLRYNLDTYELQKLKESGKOHGA 120  
 QY 157 SPSDYKWKMSADSCNMSGLTIVYLGIARVYKLFSLDQYSPPPSEPPSHRQR 216  
 Db 121 SPSDYKWKMSADSCNMSGLTIVYLGIARVYKLFSLDQYSPPPSEPPSHRQR 180  
 QY 217 FTNAGPPPPPKSEFTGPQNTGHTATSGPSAFTGQOQYENSGPGFTGTGATGILGYL 276  
 Db 181 FTNAGPPPPPKSEFTGPQNTGHTATSGPSAFTGQOQYENSGPGFTGTGATGILGYL 240  
 QY 277 FGSNRATPPSDSYPPSPYSPYSGTWNRAVSPHGGSGSYSCVNSDTKTRTASGYGCT 336  
 Db 241 FGSNRATPPSDSYPPSPYSPYSGTWNRAVSPHGGSGSYSCVNSDTKTRTASGYGCT 300  
 QY 337 RRR 339  
 Db 301 RRR 303

RESULT 4  
 QY 08R300 PRELIMINARY; PRT; 363 AA.  
 AC Q8R300; Q8N9S4;  
 DT 01-JUN-2002 (TrEMBLrel. 21, Created)  
 DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)  
 DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)  
 DE 1810045K07Rik protein (Mus musculus cDNA fls, clone  
 DE TRACH2016709).  
 GN Name=1810045K07Rik;  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 ON NCBI\_TaxID=10090;  
 RX [1]  
 SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6J; TISSUE=Mammary tumor;  
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242638999;  
 RA Strauberg R.L., Felngold E.A., Grouse L.H., Derge J.G., Schuler G.D.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buettow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh P.,  
 RA Diatchenko L., Marulisa K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.B.,  
 RA Brownstein M.J., Uedin T.B., Toshiyuki S., Carninci P., Prange C.J.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Adamson R.D., Mullany S.J.,  
 RA Bobak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Vallatton D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,  
 RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Greenwood J., Schmutz J., Myers R.M., Butlerfield Y.S.,  
 RA Krzyzanski M.I., Skaleja U., Smallus D.B., Scherch A., Schein J.E.,  
 RA Jones S.J., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 RT and mouse cDNA sequences";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 RN [2]  
 SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6J; TISSUE=Mammary tumor;  
 RA Strauberg R.;  
 RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.  
 RN [3]  
 SEQUENCE FROM N.A.  
 RC Suzuki O., Sasaki N., Aotaka S., Shoji T., Ichihara T., Shiohata N.,  
 RA Matsumoto K., Hirano M., Sano S., Nomura R., Yoshikawa Y.,  
 RA Matsumura Y., Moriya S., Chiba B., Momiyama H., Onogawa S.,  
 RA Kaeriyama S., Satoh N., Matsunawa H., Takahashi E., Katoka R.,  
 RA Kuga N., Kuroda A., Satoh I., Kamata K., Takami S., Terashima Y.,  
 RA Watanabe M., Sugiyama T., Irie R., Otsuki T., Sato H., Ota T.,  
 RA Wakamatsu A., Ishii S., Yamamoto J., Isono Y., Kawai-Hio Y., Satou K.,  
 RA Nishikawa T., Kimura K., Yamashita H., Matsumoto K., Nakamura Y.,  
 RA Sekine M., Kikuchi H., Kanda K., Magatsuna M., Morikawa K.,

RA Kanehori K., Takahashi-Fujii A., Oshima A., Sugiyama A., Kawakami B.,  
 RA Suzuki Y., Sugano S., Nagahart K., Masuo Y., Nagai K., Isogai T.;  
 RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; BC024888; AAH24888.1; -.  
 DR EMBL; AK093942; BAB04255.1; -.  
 DR MGD; MGI:1915137; 1810045K07Rik.  
 DR GO; GO:0016021; C:Integral to membrane; TMS.  
 DR InterPro; IPR009567; DUF1183.  
 DR Pfam; PF06682; DUF1183; 1.  
 SQ SEQUENCE 363 AA; 38691 MW; 0457EA29DBED3AB4 CRC64;  
 Query Match 76.0%; Score 1428; DB 2; Length 363;  
 Best Local Similarity 79.3%; Pred. No. 1.9e-100;  
 Matches 268; Conservative 25; Mismatches 37; Indels 8; Gaps 4;  
 QY 3 AACGPGAGYCLLLGLHLLFLTAGPALGMPDPMRLRDYKALTLYHYRTYRRRLDPIR 62  
 Db 33 AAVGRPRAVRCPLLLSLTLVAGPALGMPDPMRLRDYKALTLYSDRTYRRRLDPIR 92  
 QY 63 QLKCVGTAGCDSYTPRVICQKNGDGVYVQNECTDLDIAVKEKTVSCGEGYSSD 122  
 Db 93 QLKCVGTAGCBAVTPRVICQKNGDGVYVQNECTDLDIAVKEKTVSCGEGYSSD 152  
 QY 123 QYVLRGSCGLRYNLDTYELQKLKESGKOHGAFSPDYKWKMSADSCNMSGLTIVYL 182  
 Db 153 QYVLRGSCGLRYNLDTYELQKLKESGKOHGAFSPDYKWKMSADSCNMSGLTIVYL 206  
 QY 183 LGIAFVYKLFSLDQYSPPPSEPPSHRQRFTNAGPPPPPKSEFTGPQNTGHTA 242  
 Db 207 FYVLAFAVYKLFSLDQYSPPPSEPPSHRQRFTNAGPPPPPKSEFTGPQNTGHTA 266  
 QY 243 TSFPGSAFTGQOQYENSGPGFTGTGATSGPSAFTGQOQYENSGPGFTGTGATGILGYL 302  
 Db 267 SSGFGSAPF-GGQGYGSSGPGFWSGLAGLGLFSGNRAATPPSDSYPPSHSGA 325  
 QY 303 MN-RAVSPHGGSGSYSCVNSDTKTRTASGYGCTRRR 339  
 Db 326 MNSRAVSPHGGSGSYSCVNSDTKTRTASGYGCTRRR 363

RESULT 5  
 QY 08C6G7 PRELIMINARY; PRT; 334 AA.  
 AC Q8C6G7;  
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)  
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)  
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
 DE Mus musculus adult female placenta cDNA, RIKEN full-length enriched  
 DE library, clone:1600024G18 product:similar to FOAP-7.  
 GN Name=1810045K07Rik;  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 ON NCBI\_TaxID=10090;  
 RX [1]  
 SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6J; TISSUE=Placenta;  
 RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;  
 RA Carninci P., Hayashizaki Y.;  
 RT "High-efficiency full-length cDNA cloning";  
 RL Meth. Enzymol. 303:19-44(1999).  
 RN [2]  
 SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6J; TISSUE=Placenta;  
 RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;  
 RA RIKEN PANTOM Consortium;  
 RT "Functional annotation of a full-length mouse cDNA collection";  
 RL Nature 409:685-690(2001).  
 RN [3]  
 SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6J; TISSUE=Placenta;  
 RA The PANTOM Consortium;  
 RL the RIKEN Genome Exploration Research Group Phase I & II Team;

RT	"Analysis of the mouse transcriptome based on functional annotation of
RT	60,770 full-length cDNAs."
RL	Nature 420:563-573(2002).
RN	[4]
RN	SEQUENCE FROM N.A.
RP	STRAIN=C57BL/6J; TISSUE=Placenta;
RC	MEDLINE=00499374; PubMed=110421519; DOI=10.1101/gr.145100;
RA	Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA	Komuro H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT	"Normalization and subtraction of cap-trapper-selected cDNAs to
RT	prepare full-length cDNA libraries for rapid discovery of new genes.;"
RL	Genome Res. 10:1617-1630(2000).
RN	[5]
RN	SEQUENCE FROM N.A.
RP	STRAIN=C57BL/6J; TISSUE=Placenta;
RC	MEDLINE=00503091; PubMed=11076861; DOI=10.1101/gr.152600;
RA	Shibata K., Itoh M., Aizawa K., Nagaoaka S., Sasaki N., Carninci P.,
RA	Komuro H., Akiyama J., Niehi K., Kitamura T., Taishiro H., Itoh M.,
RA	Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA	Yamanoto R., Matsunoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA	Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Wataniki M.,
RA	Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsumura S., Kawai J.,
RA	Okazaki Y., Muramatsu M., Inoue Y., Kita A., Hayashizaki Y.;
RT	"RIKEN integrated sequence analysis (RISA) system-384-format
RT	sequencing pipeline with 384 multicapillary sequencer."
RL	Genome Res. 10:1757-1771(2000).
RN	[6]
RN	SEQUENCE FROM N.A.
RP	STRAIN=C57BL/6J; TISSUE=Placenta;
RC	Adachi J., Aizawa K., Akahira S., Akimura T., Aono H., Arii A.,
RA	Arai K., Bono H., Carninci P., Fukuda S., Furukoshi Y., Furuno M.,
RA	Hanagaki T., Hara A., Hayatsu N., Hiramoto K., Hirooka T., Horii F.,
RA	Iinouchi K., Ishii Y., Itoh M., Izawa M., Kasukawa T., Kato H.,
RA	Kawai J., Kojima Y., Komuro H., Kouda M., Koyasu S., Kurihara C.,
RA	Matsuyama T., Miyazaki A., Nishi K., Nomura K., Nunazaki R., Ono M.,
RA	Ozekaki Y., Okido T., Owa C., Salto R., Salto R., Sakai C., Sakai K.,
RA	Sano H., Saeki D., Shibata K., Shibata Y., Shingawa A., Shiraki T.,
RA	Sogabe Y., Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T.,
RA	Tajima Y., Toyota T., Yamamura T., Yamanaoka I., Yasuiishi A.,
RA	Yoshida K., Yoshino M., Muramatsu M., Hayashizaki Y.;
RL	Submitted (Apr-2002) to the EMBL/GenBank/DBS databases.
DR	EMBL: AK075744; BAC5924.1; -
DR	MGI: MGI1915137, 181004SK07rik
DR	GO: GO:0016021; C: integral to membrane; TMS.
DR	InterPro: IPR009567; DUF1183.
DR	Pfam: PF06682; DUF1183; 1.
SO	SEQUENCE 334 AA; 35856 MW; EA12FEA138052BCC4 CRC64;
Query Match	75.9%; Score 1427; DB 2; Length 334;
Best Local Similarity	79.3%; Pred. No.2.1e-100;
Matches 268; Conservative 25; Mismatch 37; Indels 8; Gaps 4;	
DQ	3 AACGPGAGCYLLGLHLFLTLTAGPPLAGNNDDPRMLLRVKKLTLYHRYTTSRRLDPT 62
Db	4 AAVGRPPALACPLLILSLIVAGPPLAGMNDPRILKRVKLTLYSDRTTSKRDLPT 63
DQ	OLKCVGTAGCDSYTPPVITOCNKGMVDGVDMCECTDIDIAVKFGKTIVSCGEYSSED 122
Db	64 OLKCVGTAGCAEAYTPPVITOCNKGMVDGVDMCECTDIDIAVKFGKTIVSEGEYSSED 123
DQ	123 QYLVRSGCGLENYLDTTELGLQLKLAKESGKHGFASPSDYIYKMSADSGNMGILTIVVL 182
Db	124 QYLVRSGCGLENYLDTTELGLKLKLAKESGKHQG---FSDYHNKLVSDDSC---GFTIIANL 177
DQ	183 LGIAFWVVYLFKLSDDGYSPPEVEYEPFSHRVRFNSAGRPAPRGKSFSTPOVTGGA 242
Db	178 FVLAFVAVYLFKLSDDGSPPEVPISHPYSHSRFSAAGAAPPCKSFSTPOVTGGA 237
DQ	243 TSFGFSGAFTGGQQSYENSGBGFMTGLTGGLIGLTFGSNAATPFSDSWYPPSPYSGT 302
Db	238 SSFGFSGAF--CGCGYGSSGGEFGMSGLAGGLGLTLPSSNDAAPFDSDSWHYPPSHSGA 296
DQ	303 WNV-RAYSPLHGSGSYSCVCSNDDTKTRTVASGCGTERR 339

297 WNSRAIYSPUGGAGSTICASSNDSRRTASGVTGTRR 334

Db

RESULT 6

09D8R1

AD 09D8R1 PRELIMINARY; PRT; 363 AA.

IC 09D8R1;

DT 01-JUN-2001 (TRMBLrel. 17, Created)

DT 01-JUN-2001 (TRMBLrel. 17, Last sequence update)

DT 05-JUN-2004 (TRMBLrel. 27, Last annotation update)

DE Mus musculus 10 day old male pancreas cDNA, RIKEN full-length enriched library, clone:1810045K07 product:similar to FOXP-7 (1810045K07Rik protein).

DS Name=1810045K07Rik;

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murine; Mus.

OX NCBI\_TaxID=10090;

LN [1]

RN SEQUENCE FROM N.A.

RP STRAIN=C57BL/6J; TISSUE=Pancreas;

RC MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;

RX Carninci P., Hayashizaki Y.;

RA "High-efficiency full-length cDNA cloning.";

RT Mech. Enzymol. 303:19-44(1999).

RL [2]

RN SEQUENCE FROM N.A.

RP STRAIN=C57BL/6J; TISSUE=Pancreas;

RC MEDLINE=1085660; PubMed=11217851; DOI=10.1038/35055500;

RX RIKEN FANTOM Consortium;

RA "Functional annotation of a full-length mouse cDNA collection.";

RT Nature 409:685-690(2001).

RL [3]

RN SEQUENCE FROM N.A.

RP STRAIN=C57BL/6J; TISSUE=Pancreas;

RC The FANTOM Consortium;

RA the RIKEN Genome Exploration Research Group Phase I & II Team;

RT "Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs.";

RL Nature 420:563-573(2002).

RN [4]

RN SEQUENCE FROM N.A.

RP STRAIN=C57BL/6J; TISSUE=Pancreas;

RC MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;

RX Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M., Kono H., Okazaki Y., Muramatsu M., Hayashizaki Y.;

RA "Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes.";

RT Genome Res. 10:1617-1630(2000).

RL [5]

RN SEQUENCE FROM N.A.

RP STRAIN=C57BL/6J; TISSUE=Pancreas;

RC MEDLINE=205010913; PubMed=11076661; DOI=10.1101/gr.152600;

RX Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P., Kono H., Akiyama J., Nishi K., Kitsuai T., Tashiro H., Itoh M., Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A., Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kaishiwagi K., Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M., Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuda S., Kawai J., Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;

RT "RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multiplexed capillary sequencer.";

RL Genome Res. 10:1757-1771(2000).

RN [6]

RN SEQUENCE FROM N.A.

RP STRAIN=C57BL/6J; TISSUE=Pancreas;

RC Aachai J., Aizawa K., Akahira S., Akimura T., Arai A., Aono H., Arakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M., Hanagata T., Hara A., Hayatsu N., Hiramoto K., Hirooka T., Hori F., Imotani K., Ishii Y., Itoh M., Izawa M., Kasukawa T., Kato H., Kawai J., Kojima Y., Kono H., Kouda M., Koya S., Kurihara C., Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numazaki R., Ohno M.,

RA Okazaki Y., Okido T., Owa C., Saito H., Saito R., Sakai C., Sakai K.,  
 RA Sano H., Saeki D., Shibata K., Shibata Y., Shingawa A., Shiraki T.,  
 RA Sogabe Y., Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T.,  
 RA Tajima Y., Toya T., Yamamura T., Yasunishi A., Yoshida K., Yoshino M.,  
 RA Muramatsu M., Hayashizaki Y.,  
 RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.

RP SEQUENCE FROM N.A.

RC STRAIN=FVB/N; TISSUE=Kidney;  
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Strausberg R.L.; Feingold E.A.; Grouse L.H.; Derge J.G.,  
 RA Klausner R.D.; Collins F.S.; Wagner L.; Shenmen C.M.; Schuler G.D.,  
 RA Altschul S.F.; Zeeberg B.; Buetow K.H.; Schaefer C.F.; Bhat N.K.,  
 RA Hopkins R.F.; Jordan H.; Moore T.; Max S.I.; Wang J.; Hsieh F.,  
 RA Diachenko L.; Marusina K.; Farmer A.A.; Rubin G.M.; Hong L.,  
 RA Scapleton M.; Soares M.B.; Bonaldo M.F.; Casavant T.L.; Scheetz T.E.,  
 RA Brownstein M.J.; Udell T.B.; Tohiyuki S.; Carninci P.; Prange C.,  
 RA Raba S.S.; Loguallano N.A.; Peters G.J.; Abramson R.D.; Mullaly S.J.,  
 RA Bosak S.A.; McGowan P.J.; McKernan K.J.; Malek J.A.; Gunaratne P.H.,  
 RA Richards S.; Worley K.C.; Hale S.; Garcia A.M.; Gay L.J.; Hulyk S.W.,  
 RA Villalón D.K.; Muzny D.M.; Sodergren E.J.; Lu X.; Gibbs R.A.,  
 RA Fahy J.; Helton E.; Kettman M.; Madan A.; Rodriguez S.; Sanchez A.,  
 RA Whiting M.; Madan A.; Young A.C.; Shevchenko Y.; Bouffard G.G.,  
 RA Blakeley R.W.; Touchman J.W.; Green E.D.; Dickson M.C.,  
 RA Rodriguez A.C.; Grimwood J.; Schmutz J.; Myers R.M.; Butcherfield Y.S.,  
 RA Krzywinski M.I.; Skalska U.; Smalins D.E.; Schnerch A.; Schein J.E.,  
 RA Jones S.J.; Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 RT and mouse cDNA sequences";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

RP SEQUENCE FROM N.A.

RC STRAIN=FVB/N; TISSUE=Kidney;  
 RA Strausberg R.;  
 RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AK007787; BAB25254.1; -  
 DR EMBL; BC013497; AAH13497.1; -  
 DR MGD; MGI:1915137; 1810045K07Rik.  
 DR GO; GO:0016021; C:Integral to membrane; TMS.  
 DR Interpro; IPR009567; DUF1183.  
 DR Pfam; PF06682; DUF1183; 1.  
 SQ SEQUENCE 363 AA; 38705 MW; 463BCB5E1080CF5 CRC64;

Query Match 75.9%; Score 1427; DB 2; Length 363;  
 Best Local Similarity 79.3%; Pred. No. 2.3e-100;  
 Matches 268; Conservative 25; Mismatches 37; Indels 8; Gaps 4;

QY 3 AACGPAAGYCLLGLHFLITAGPALGMDPRMLRDVKALTLHYDRYTSRRLLPIP 62  
 DB 33 AAVGRPALRCPLLLLSLLVAGPALGMDPRILRLDKALTLVSDRTTSRRLLPIP 92  
 QY 63 QLKCVGTAGCDSTPRVIOCNKMGWDYDVQVECKTDLDIAVYFGKTVVSCGEYSSSD 122  
 DB 93 QLKCVGTAGCAATPRVIOCNKMGWDYDVQVECKTDLDIAVYFGKTVVSCGEYSSSD 152  
 QY 123 QYTLRGSGLENYLDYTELGLQKLKESGKHGAFASPDYTYKSSADSCMSGLITTVL 182  
 DB 153 QYTLRGSGLENYLDYTELGLKKLKESGKHG--FSDYYHKLYSSDSC--GPIITAVL 206  
 QY 183 LGIAFVYVYKFLPSDGOYSPPEYSEYPPFSRHYORFTNSAGPPPGPKSFTGPONTGHA 242  
 DB 207 FVLAFAVYVYKFLPSDGOYSPPEYSEYPPFSRHYORFTNSAGPPPGPKSFTGPONTGHA 266  
 QY 243 TSGFGSAFTGQGYENSGPFGFTGLGTGGLGLYLFSGSNRAATPFSDSWYPPSYPGT 302  
 DB 267 SSGFGSAF-GGQGYGSGPFGFTGLGTGGLGLYLFSGSNRAATPFSDSWYPPSYPGT 325  
 QY 303 WN-RAVYPLHGSGSYVCSNSDPTKTRTASGYGCTRRR 339  
 DB 326 WNSRAVYPLHGSGSYVCSNSDPTKTRTASGYGCTRRR 363

RESULT 7

08R233 PRELIMINARY; PRT; 363 AA.

AC 08R233;  
 DT 01-JUN-2002 (TEMBUREL 21, Created)  
 DT 01-JUN-2002 (TEMBUREL 21, Last sequence update)  
 DT 01-MAR-2004 (TEMBUREL 26, Last annotation update)  
 DE 1810045K07Rik protein.  
 GN Name=1810045K07Rik.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 NX NCBI\_TaxID=10090;  
 RX [1]

RP SEQUENCE FROM N.A.  
 RC STRAIN=FVB/N; TISSUE=Salivary gland;  
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Strausberg R.L.; Feingold E.A.; Grouse L.H.; Derge J.G.,  
 RA Klausner R.D.; Collins F.S.; Wagner L.; Shenmen C.M.; Schuler G.D.,  
 RA Altschul S.F.; Zeeberg B.; Buetow K.H.; Schaefer C.F.; Bhat N.K.,  
 RA Hopkins R.F.; Jordan H.; Moore T.; Max S.I.; Wang J.; Hsieh F.,  
 RA Diachenko L.; Marusina K.; Farmer A.A.; Rubin G.M.; Hong L.,  
 RA Scapleton M.; Soares M.B.; Bonaldo M.F.; Casavant T.L.; Scheetz T.E.,  
 RA Brownstein M.J.; Udell T.B.; Tohiyuki S.; Carninci P.; Prange C.,  
 RA Raba S.S.; Loguallano N.A.; Peters G.J.; Abramson R.D.; Mullaly S.J.,  
 RA Bosak S.A.; McGowan P.J.; McKernan K.J.; Malek J.A.; Gunaratne P.H.,  
 RA Richards S.; Worley K.C.; Hale S.; Garcia A.M.; Gay L.J.; Hulyk S.W.,  
 RA Villalón D.K.; Muzny D.M.; Sodergren E.J.; Lu X.; Gibbs R.A.,  
 RA Fahy J.; Helton E.; Kettman M.; Madan A.; Rodriguez S.; Sanchez A.,  
 RA Whiting M.; Madan A.; Young A.C.; Shevchenko Y.; Bouffard G.G.,  
 RA Blakeley R.W.; Touchman J.W.; Green E.D.; Dickson M.C.,  
 RA Rodriguez A.C.; Grimwood J.; Schmutz J.; Myers R.M.; Butcherfield Y.S.,  
 RA Krzywinski M.I.; Skalska U.; Smalins D.E.; Schnerch A.; Schein J.E.,  
 RA Jones S.J.; Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 RT and mouse cDNA sequences";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

RP SEQUENCE FROM N.A.  
 RC STRAIN=FVB/N; TISSUE=Salivary gland;  
 RA Strausberg R.;  
 RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; BC022616; AAH22616.1; -  
 DR MGD; MGI:1915137; 1810045K07Rik.  
 DR GO; GO:0016021; C:Integral to membrane; TMS.  
 DR Interpro; IPR009567; DUF1183.  
 DR Pfam; PF06682; DUF1183; 1.  
 SQ SEQUENCE 363 AA; 38747 MW; A99A614440A91E84 CRC64;

Query Match 75.5%; Score 1418; DB 2; Length 363;  
 Best Local Similarity 79.0%; Pred. No. 1.1e-99;  
 Matches 267; Conservative 25; Mismatches 38; Indels 8; Gaps 4;

QY 3 AACGPAAGYCLLGLHFLITAGPALGMDPRMLRDVKALTLHYDRYTSRRLLPIP 62  
 DB 33 AAVGRPALRCPLLLLSLLVAGPALGMDPRILRLDKALTLVSDRTTSRRLLPIP 92  
 QY 63 QLKCVGTAGCDSTPRVIOCNKMGWDYDVQVECKTDLDIAVYFGKTVVSCGEYSSSD 122  
 DB 93 QLKCVGTAGCAATPRVIOCNKMGWDYDVQVECKTDLDIAVYFGKTVVSCGEYSSSD 152  
 QY 123 QYTLRGSGLENYLDYTELGLQKLKESGKHGAFASPDYTYKSSADSCMSGLITTVL 182  
 DB 153 QYTLRGSGLENYLDYTELGLKKLKESGKHG--FSDYYHKLYSSDSC--GPIITAVL 206  
 QY 183 LGIAFVYVYKFLPSDGOYSPPEYSEYPPFSRHYORFTNSAGPPPGPKSFTGPONTGHA 242  
 DB 207 FVLAFAVYVYKFLPSDGOYSPPEYSEYPPFSRHYORFTNSAGPPPGPKSFTGPONTGHA 266  
 QY 243 TSGFGSAFTGQGYENSGPFGFTGLGTGGLGLYLFSGSNRAATPFSDSWYPPSYPGT 302  
 DB 267 SSGFGSAF-GGQGYGSGPFGFTGLGTGGLGLYLFSGSNRAATPFSDSWYPPSYPGT 325  
 QY 303 WN-RAVYPLHGSGSYVCSNSDPTKTRTASGYGCTRRR 339

Db 326 WNSRAYSPGCGAGSYCASSNADSRRTTAGYGTGRR 363

RESULT 8

Q6AYN2 PRELIMINARY; PRT; 334 AA.

AC 06AYN2; 25-OCT-2004 (TrEMBLrel. 28, Created)

DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)

DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)

DE Hypoetical protein MGC33866.

GN Name=MGC33866;

OS Rattus norvegicus (Rat).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

OX NCBI\_TaxID=10116;

RA Rattus norvegicus (Rat).

RP TISSUE=Testis;

RC PubMed=12477932; DOI=10.1073/pnas.2426038999;

RX Strausberg R.L., Peingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buettow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heile F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldi M.F., Casavant T.L., Schetz T.E., Brownstein M.J., Ustin T.B., Toshlyuki S., Carninci P., Prange C., Rana S.S., Loughran N.A., Peters G.J., Abramson R.D., Mullaly S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Whiting J., Helton A., Kettman M., Madan A., Rodriguez S., Sanchez A., Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Myers R.M., Butterfield Y.S., Krzyviński M.I., Skalka U., Smalios D.E., Schnerch A., Schein J.E., Jones S.J., Marra M.A.;

RA "Generation and initial analysis of more than 15,000 full-length human RT and mouse cDNA sequences."

RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

RL [2]

RN SEQUENCE FROM N.A.

RC TISSUE=Testis;

RP Director MGC Project;

RU Submitted (Aug-2004) to the EMBL/GenBank/DBJ databases.

DR EMBL: BC078979; AAH78979.1; -.

DR InterPro: IPR009567; DUF1183.

DR Pfam: PF06682; DUF1183; 1.

KW Hypoetical protein.

SO SEQUENCE 334 AA; 35885 MW; 6812CFBA8D352DC CRC64;

Query Match 73.8%; Score 1387; DB 2; Length 334;

Best Local Similarity 76.6%; Pred. No. 2.3e-97;

Matches 259; Conservative 28; Mismatches 43; Indels 8; Gaps 4;

QY 3 AACGPGAGCCLGHLPLTGPALGMDPRMDKALTLHYDRYTSRRDPP 62

DB 4 AAGRPAPARCLLLLSPLLVAGPALCMKPNRILRLDVALTLSDRTYTSRRDPP 63

QY 63 QLKCVGATAGCDSYTPRVICQKNGMDYDQWCKTDLDIAVKGFTVSCGYESSED 122

DB 64 QLKCVGATAGCDAVTPRVVCGQKMGDYDQWCKTDLDIAVKGFTVSCGYESSED 123

QY 123 QYVLRSGCGELVLDYTELGLQKLGSGKQHGFAFSFDYTYKSSADSCMSGLITTVL 182

DB 124 QYVLRSGCGELVLDYTELGLQKLGSGKQHGFAFSFDYTYKSSADSCMSGLITTVL 177

QY 183 LGIAFVYVYKFLSLDSGYSPRPYSEYRSHRYORFNTNSGRRPGRKSFRTGPNNGKA 242

DB 178 FVLAFFVYVYKFLSLDSGYSPRPYSEYRSHRYORFNTNSGRRPGRKSFRTGPNNGKA 237

QY 243 TSGFGSAFTGCGYENSGRPFMTGLGTGILGYLFGSNRAATPFSDSWYPSYPSYPT 302

Db 238 SSGFGSAF-CGGSYASSGPGFWSGLGAGLLLYLFGSNRAATPFSDSWYPSYPSYACA 296

QY 303 WN-RAYSPHGGSGSYVCSNDDTKRTTAGYGTGRR 339

Db 297 WNSHAYSPGCGAGSYCASSNADSRRTTAGYGTGRR 334

RESULT 9

Q8C2P1 PRELIMINARY; PRT; 292 AA.

AC Q8C2P1; 01-MAR-2003 (TrEMBLrel. 23, Created)

DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)

DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)

DE Mus musculus 2 days neonate thymus thymic cells cDNA, RIKEN full-length enriched library, clone: B430024120 product: similar to FOAP-7 (fragment).

GN Name=1810045K07R1K;

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI\_TaxID=10090;

RA Rattus norvegicus (Rat).

RP TISSUE=Thymus;

RC MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;

RX Strausberg R.L., Peingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buettow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heile F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldi M.F., Casavant T.L., Schetz T.E., Brownstein M.J., Ustin T.B., Toshlyuki S., Carninci P., Prange C., Rana S.S., Loughran N.A., Peters G.J., Abramson R.D., Mullaly S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Whiting J., Helton A., Kettman M., Madan A., Rodriguez S., Sanchez A., Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Myers R.M., Butterfield Y.S., Krzyviński M.I., Skalka U., Smalios D.E., Schnerch A., Schein J.E., Jones S.J., Marra M.A.;

RA "High-efficiency full-length cDNA cloning."

RT Meth. Enzymol. 303:19-44(1999).

RL [2]

RN SEQUENCE FROM N.A.

RC STRAIN=NOD; TISSUE=Thymus;

RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;

RA RIKEN FANTOM Consortium;

RT "Functional annotation of a full-length mouse cDNA collection."

RL Nature 409:685-690(2001).

RN [3]

RN SEQUENCE FROM N.A.

RC STRAIN=NOD; TISSUE=Thymus;

RA The FANTOM Consortium;

RT "Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs."

RL Nature 420:563-573(2002).

RN [4]

RN SEQUENCE FROM N.A.

RC STRAIN=NOD; TISSUE=Thymus;

RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/97.145100;

RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M., Kono H., Okazaki Y., Muramatsu M., Hayashizaki Y.;

RT "Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes."

RL Genome Res. 10:1617-1630(2000).

RN [5]

RN SEQUENCE FROM N.A.

RC STRAIN=NOD; TISSUE=Thymus;

RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/97.152600;

RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P., Kono H., Akiyama J., Nishi K., Katsunai T., Tashiro H., Itoh M., Sumi N., Ishii Y., Nakamura S., Hazama M., Nishino T., Harada A., Yamamoto S., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K., Fujitake S., Inoue K., Togawa Y., Izawa M., Ohara E., Wachihi K., Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsura S., Kawai J., Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;

RT RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multiplexed capillary sequencer."

RL Genome Res. 10:1757-1771(2000).

RN [6]

RN SEQUENCE FROM N.A.

RC STRAIN=NOD; TISSUE=Thymus;

RA Adachi S., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P., Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,

RA Hayashida K., Hayatsu N., Hiramoto K., Hirooka T., Hirozane T.,  
 RA Hori F., Imocant K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,  
 RA Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,  
 RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,  
 RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohnato N., Okazaki Y.,  
 RA Saito R., Saitoh H., Sakai C., Sakai T., Sakazume N., Sano H.,  
 RA Sasaki D., Shibata K., Shingawa A., Shiraki T., Sogabe Y., Tgamai M.,  
 RA Tagawa A., Takahashi P., Takaku-Akahira S., Takeda Y., Tanaka T.,  
 RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.,  
 RL EMBL; AK088728; BAC40531.1; -  
 DR MGD; MGI:1915137; 1810045K07R1k.  
 DR GO; GO:0016021; C: integral to membrane; TAS.  
 DR InterPro; IPR009567; DUF1183.  
 DR Pfam; PF06682; DUF1183; 1.  
 DR NON TER 1  
 SQ SEQUENCE 292 AA; 31362 MW; 580900AEP9294C68 CRC64;

Query Match 63.6%; Score 1176.5; DB 2; Length 292;  
 Best Local Similarity 79.9%; Pred. No. 2e-81;  
 Matches 223; Conservative 18; Mismatches 31; Indels 7; Gaps 3;

QY 3 AACGPGAGYCLLGLGLPLTAGPALGMNDPDRMLRDYKALTLHYDRYTSRLDPIR 62  
 DB 21 AAGRPAAVRCPLLLLSLLLVAGPALGMNDPDRILRDYKALTLVSDRTTSRLDPIR 80  
 QY 63 QLKCVGCTAGCDSYTPKVIQCNKMGDYGVDWECKTDLDAIYKGTIVSCEGSSSED 122  
 DB 81 QLKCVGCTAGCBAATPRVICOQKMGDYGVDWECKTDLDAIYKGTIVSCEGSSSED 140  
 QY 123 QYVLRGSCGLENYLDYELGLQKESGKHGFPASPDYKYKSSADSCNMSGILITVVL 162  
 DB 141 QYVLRGSCGLENYLDYELGLQKESGKHGFPASPDYKYKSSADSCNMSGILITVVL 194  
 QY 183 LGIAFVYVYKPLFLSDGQYSPPEYSEYPPSHRYQFTNSAGPPPGFKSEFTGQNTGCA 242  
 DB 195 FVLAFAVYKPLFLSDGQSPPEYSEYPPSHRYQFTNSAGPPPGFKSEFTGQNTGCA 254  
 QY 243 TSGFGSAFTGQCGYENSQPGFTGTLGTGILGYLFGSNR 281  
 DB 255 SSGFGSNAF-CGGQYSSGPGFMSGIGLAGGLGYLFGSNR 292

RESULT 10  
 Q22254 PRELIMINARY; PRT; 323 AA.  
 AC Q22254;  
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
 DE Hypothetical protein T06D8.9.  
 GN ORFName=T06D8.9;  
 OS Caenorhabditis elegans.  
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditicoidea;  
 OC Rhabditidae; Pelodierinae; Caenorhabditis.  
 OC NCB1\_TaxID=6239;  
 OX 11  
 RP SEQUENCE FROM N.A.  
 RP STRAIN=Br1stcol N2;  
 RX MEDLINE=99069613; PubMed=9851916;  
 RA none;  
 RT "Genome sequence of the nematode C.elegans: A platform for  
 RT investigating biology."  
 RT Science 282:2012-2018(1998).  
 RN 12  
 RP SEQUENCE FROM N.A.  
 RP STRAIN=Br1stcol N2;  
 RA Palmer S.;  
 RL Submitted (APR-1995) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; Z49130; CA88972.1; -  
 DR PIR; T24582; T24582.  
 DR WormBase; WBGene00011529; T06D8.9.  
 DR WormBep; T06D8.9; CE02330.

DR InterPro; IPR009567; DUF1183.  
 DR Pfam; PF06682; DUF1183; 1.  
 KW Hypothetical protein.  
 SQ SEQUENCE 323 AA; 34010 MW; 718BF6B22FE2D084 CRC64;

Query Match 26.6%; Score 499.5; DB 2; Length 323;  
 Best Local Similarity 34.8%; Pred. No. 6.6e-30;  
 Matches 120; Conservative 40; Mismatches 88; Indels 97; Gaps 9;

QY 35 DRMLRDYKALTLHYDRYTSRLDPIQLKCVGCTAGCDSYTPKVIQCNKMGDYGVD 94  
 DB 36 DKVLADVSAITLHKQKMTTGRVRVPTQLKCVGSGAK-GAIPKVVQCANGQFDSVDQ 94  
 QY 95 WECKTDLDAIYKGTIVSCEGSSSEDQYVLRGSGLENYMDYTL-GLQKESGKH 153  
 DB 95 WRCDADLPDMEFGSISVCEGYADDPYILNGSGLENYELRYNSASGNRSVRSQD 154  
 QY 154 GFASPSDYKYKSSADSCNMSGILITVVLGIAFVYVYKPLFLSDQ----- 198  
 DB 155 RWDQFA-----TPVVAFLIYIYAMWTRNQNPBSSGYTSGSGCP 196  
 QY 199 -----YSPPEYSEYPPSHRYQFTNSAGPPPGFKSEFT--GPQNTG 239  
 DB 197 GPGSGSGGGGPGGYSPAPPPDY-----SKPPEYGRGDSQSGGCGSS 243  
 QY 240 HGATSGFGSAFTGQCGYENSQPGFTGTLGTGILGYLFGS-----NRATPDSMTYPS 294  
 DB 244 SGGASGSGA-----NNGGSFMTGASIGALGGYLAASFNNNAVYAR----- 285  
 QY 295 YPSPYSGTWNRAVPLHGGSGSYSCNSDTKRTAGYGGTERR 339  
 DB 286 -----RNRKGFQDTGFSSSDSMSBSTSMRSSSGIGGTTKR 323

RESULT 11  
 Q75303 PRELIMINARY; PRT; 357 AA.  
 AC Q75303;  
 DT 01-MAR-2004 (TrEMBLrel. 26, Created)  
 DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)  
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
 DE Hypothetical protein.  
 GN Name=NCU07545.1;  
 OS Neurospora crassa.  
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;  
 OC Sordariomycetidae; Sordariales; Sordariaceae; Neurospora.  
 OX 11  
 RN 11  
 RP SEQUENCE FROM N.A.  
 RP STRAIN=OR74A;  
 RC Galagan J.E., Calvo S.E., Borkovich K.A., Selker E.U., Read N.D.,  
 RA Jaffe D., Fitzhugh W., Ma L.-J., Smirnov S., Puccell S., Rehman B.,  
 RA Kline T., Engels R., Wang S., Nielsen C.B., Butler J., Endrizzi M.,  
 RA Cui D., Iankiev P., Pedersen D., Nelson M., Washburne M.,  
 RA Selitrenikoff C.P., Kinsey J.A., Braun E.L., Zelter A., Schulte U.,  
 RA Kothe G.O., Jedd G., Mewes W., Staben C., Marcotte B., Greenberg D.,  
 RA Roy A., Foley K., Naylor J., Thomann N., Barrett R., Gierre S.,  
 RA Kamal M., Kamysseilis M., Mauceli B., Bielke C., Rudd S., Fishman D.,  
 RA Kyselofova S., Raamsen C., Metzberg R.L., Perkins D.D., Kroken S.,  
 RA Cogoni C., Macino G., Carcheside D., Li W., Pratt R.J., Omani S.A.,  
 RA Desouza C.C., Glaes L., Orbach M.J., Berglund J., Voelker R.,  
 RA Varden O., Plamann M., Seiler S., Dunlap J., Radford A., Aramayo R.,  
 RA Natvig D.O., Alex L.A., Mannhaupt G., Ebbold D.J., Freitag M.,  
 RA Paulsen I., Sachs M.S., Lander B.S., Nussbaum C., Birren B.,  
 RT "The Genome Sequence of the Filamentous Fungus Neurospora crassa."  
 RT Nature 0:0-0(2003).  
 CC -1- CAUTION: The sequence shown here is derived from an  
 CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is  
 CC preliminary data.  
 DR EMBL; AABX01000415; EAA29822.1; -  
 DR InterPro; IPR009567; DUF1183.  
 DR Pfam; PF06682; DUF1183; 1.  
 KW Hypothetical protein.





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Db 685 -----PESADPRHASPRTDXYGSRPSSSGVSSGSGPSPAPAS--FGYH 730
QY 237 NTGHGATSGFGSAFTGQGGY-ENSGPGFMTGLGTGILGYPGSNRAATPPSDSMY---- 291
Db 731 HGHQAYEGSSSSYPSPYSGSGSPSY-----GSSSGSPSYG-----PSCPSYSQSP 778
QY 292 ----YPSY--PSPYGTMTNRAVSLHGGSSGSYSVCSNSDTRKTATAGYGG 335
Db 779 SYSQSPSYGAPSPQPPYGSQ---PHYGGPHSSYSGGRPPSPPPSGYGG 825

RESULT 14
08X005 PRELIMINARY; PRT; 977 AA.
ID 08X005
AC 08X005;
DT 01-MAR-2002 (TREMBlrel. 20, Created)
DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE Glycine rich protein (Het-COR).
GN Name=B2JH20.080;
OS Neurospora crassa.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Sordariomycetidae; Sordariales; Sordariaceae; Neurospora.
OX NCBI_Taxid=5141;
CX [1]
RP SEQUENCE FROM N.A.
RA Schulte U., Algen V., Hohelsel J., Brandt P., Fartmann B., Holland R.,
RA Nykatura G., Mewes H.W., Mannhaupt G.;
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA German Neurospora genome project;
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL669988; CAD21080.1; -.
DR Pfam; PF07217; Het-C; 1.
SQ SEQUENCE 977 AA; 104015 MW; 3E1FFABBD091E93 CRC64;

Query Match 6.6%; Score 124; DB 2; Length 977;
Best Local Similarity 22.4%; Pred. No. 0.77;
Matches 65; Conservative 38; Mismatches 99; Indels 88; Gaps 14;

QY 93 VOMECTDLDIAKFGKTVVSCGYESSBOYVLRG-----SCGLR----- 133
Db 588 VQMSRETHNDY-----KTLASBSVKEGHN-HVNLNGQPMNRGPGGHTSCGADGGHGKVA 641
QY 134 -----YNLDYTEL-----GLQKLKESGKHGFPASPSDYVKMSSADSQMSGLITI 179
Db 642 GSLMSKIGSRDLDTSA.PSGGVGGGRPSSSTGHKCYGASSSHHEVPTHGSAAY----- 695
QY 180 VVLLGIAPVVYKLP.LSDGQYSPPPYSBY--PPSHRYQRFTNSAGRPFPKSEFTGPQ 236
Db 696 -----PSSADPRHASPRTDXYGSRPSSSGVSSGSGPSPAPAS--FGYH 741
QY 237 NTGHGATSGFGSAFTGQGGY-ENSGPGFMTGLGTGILGYPGSNRAATPPSDSMY---- 291
Db 742 HGHQAYEGSSSSYPSPYSGSGSPSY-----GSSSGSPSYG-----PSCPSYSQSP 778
QY 292 ----YPSY--PSPYGTMTNRAVSLHGGSSGSYSVCSNSDTRKTATAGYGG 335
Db 790 SYSQSPSYGAPSPQPPYGSQ---PHYGGPHSSYSGGRPPSPPPSGYGG 825

RESULT 15
09UVL3 PRELIMINARY; PRT; 974 AA.
ID 09UVL3
AC 09UVL3;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE Heterokaryon incompatibility protein HET-C.
GN Name=het-C;
OS Neurospora crassa.

```

```

OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Sordariomycetidae; Sordariales; Sordariaceae; Neurospora.
OX NCBI_Taxid=5141;
CX [1]
RP SEQUENCE FROM N.A.
RA STRAIN=FGSC 2190;
RX MEDLINE=98445383; PubMed=9770498; DOI=10.1073/pnas.95.21.12398;
RA Wu J., Saupé S.J., Glass N.L.;
RT "Evidence for balancing selection operating at the het-c heterokaryon
RT incompatibility locus in a group of filamentous fungi.";
RL Proc. Natl. Acad. Sci. U.S.A. 95:12398-12403(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=FGSC 2190;
RX MEDLINE=97403306; PubMed=9258675;
RA Saupé S.J., Glass N.L.;
RT "Allelic specificity at the het-c heterokaryon incompatibility locus
RT of Neurospora crassa is determined by a highly variable domain.";
RL Genetics 146:1299-1309(1997).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=FGSC 2190;
RA Saupé S.J., Glass N.L.;
RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF195874; AAF08294.1; -.
DR InterPro; IPR008927; 6DSGH_C1-like.
DR InterPro; IPR010816; Het-C.
DR Pfam; PF07217; Het-C; 1.
SQ SEQUENCE 974 AA; 103728 MW; 2EB3D1E3D677483 CRC64;

Query Match 6.5%; Score 122; DB 2; Length 974;
Best Local Similarity 20.7%; Pred. No. 1.1;
Matches 84; Conservative 45; Mismatches 127; Indels 150; Gaps 21;

QY 31 WNDPD-----RYLTDVVALTLHYRYYTTSRLDIPQLKCYGATAG--CDSYTPRVIQ 82
Db 503 WNPDCDNPHTSHLSKD-----HFTNINLS-----CGRVAANIYQVVRVRYV 546
QY 83 CONKMGD-----YD-----VOMECTDLDIAKFG 108
Db 547 ----AMENPGVDPDSVILADVLOVFNHRAVYKQEBIQRMTYDTPVQMSRETHNDY----- 597
QY 109 KTVVSCGYESSBOYVLRG-----SCGLR-----YTELGLQKLKESG 150
Db 598 KCLLDBESVKEGHN-HVNLNGQPMNRGPGGHTSCGADGGHGKVA.GSLMSKIGSRDLDTSA 656
QY 151 KQHGK-----ASPSDYVKMSSADSQMSGLITI.VVLLGIAPVVYKLP.LSDGQYSPPPYS 205
Db 657 PSGGVGGGRPSSSTGHKCYGASSSHHE-----VTHGSAAYFS--SADPRHASPRTD 708
QY 206 EY----PPSHRYQRFTNSAGRPFPKSEFTGPONTGHGATSGFGSAFTGQGGY-NSGP 261
Db 709 RYVGSRPSSSGVSSVHSGGRSPAPGS--FGYHGHQAYEGSSSSYPSPYSGSGSPSY 766
QY 262 GFW--TGLTGLGILGYPGSNRAATPPSDSMYTPP-----PSPYGTMTNRAV----- 308
Db 767 YSGSSGSPYGYSPSPYSGSPSYQPSYGAHPSPQPPHYGSPHYGSPHYGSPHYGSPHYGSP 826
QY 309 -----PLHGSGSYSVCSNSDTRKTATAGYGG 335
Db 827 PRPSPGYGGYAGYAGAPPPSHGGYGGY-----GGYGG 859

Search completed: July 14, 2005, 20:32:13
Job time : 118.243 secs

```

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: July 14, 2005, 19:54:41 ; Search time 76.9612 Seconds

(without alignments)  
1196.043 Million cell updates/sec

Title: US-10-019-151C-1

Sequence: 1 MILLVILAFILKQVDMLESI.....AQCCMGKQKQAQVWEGTNGAS 238

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database : A\_GeneSeq\_16Dec04:\*  
1: geneseqp1980s:\*  
2: geneseqp1980s:\*  
3: geneseqp2000s:\*  
4: geneseqp2001s:\*  
5: geneseqp2002s:\*  
6: geneseqp2003as:\*  
7: geneseqp2003bs:\*  
8: geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1243	100.0	238	4	AAB20089	Aab20089 Human hyd
2	1178	94.8	638	8	ADQ96030	Adq96030 T cell ac
3	1178	94.8	638	8	ADQ96032	Adq96032 T cell ac
4	1178	94.8	1070	6	AD455285	Ad455285 Human pro
5	1178	94.8	1096	3	AAB43253	Aab43253 Human ORF
6	1178	94.8	1553	8	ADQ96036	Adq96036 T cell ac
7	1178	94.8	1726	2	AA023377	Aa023377 Polypepti
8	1178	94.8	2141	5	ABB81196	Abb81196 Human FNI
9	1178	94.8	2376	6	ABR58313	AbR58313 BC0586 P
10	1178	94.8	2376	8	ADQ96034	AdQ96034 T cell ac
11	983	79.1	1167	8	ADQ08792	AdQ08792 Ciona int
12	982	79.0	354	4	ABG04093	AbG04093 Novel hum
13	951	76.5	873	4	AAM93552	Aam93552 Human pol
14	951	76.5	873	8	ADL31282	AdL31282 Human pro
15	873	70.2	1766	4	ABBS5631	AbB5631 Drosophila
16	653	52.5	2500	8	ADN21107	Adn21107 Bacterial
17	603	48.5	316	6	ABR52630	AbR52630 Protein s
18	603	48.5	316	7	ADK64762	AdK64762 Disease t
19	603	48.5	316	8	ADN06059	Adn06059 Antiporci
20	601.5	46.8	1248	4	ABG19706	AbG19706 Novel hum
21	581.5	46.8	178	6	ABO01269	AbO01269 Growth de
22	459	36.9	89	4	ABG02994	AbG02994 Novel hum
23	356.5	28.7	1283	8	ADG24334	AdG24334 Bacterial
24	352.5	28.4	1945	8	ADR86432	AdR86432 Aspergill
25	318.5	25.6	2016	8	ADP99054	Adp99054 C. albica

26	317	25.5	2100	8	ADN19489	Adn19489 Bacterial
27	270.5	21.8	328	4	ABG04094	AbG04094 Novel hum
28	256	20.6	1610	8	ADN20795	Adn20795 Bacterial
29	237	19.1	52	4	ABG19704	AbG19704 Novel hum
30	234	18.8	60	3	AAQ02630	AaQ02630 Human sec
31	231.5	18.6	2108	8	ADN18884	Adn18884 Bacterial
32	107.5	8.6	2000	6	ABR52606	AbR52606 Protein s
33	107.5	8.6	2000	6	ADK63610	AdK63610 Disease t
34	88.5	7.1	410	6	ABU33498	AbU33498 Protein e
35	87.5	7.0	4624	7	ADP78572	AdP78572 Dynein ax
36	87.5	7.0	4624	7	ADJ71185	AdJ71185 Human hea
37	86	6.9	252	6	ABM71071	AbM71071 Staphyloc
38	86	6.9	396	6	ABM70942	AbM70942 Staphyloc
39	86	6.9	414	6	ABU42356	AbU42356 Protein e
40	85.5	6.9	1318	8	ADL05937	AdL05937 M. catarr
41	85.5	6.9	2173	5	ABP69251	AbP69251 Human pol
42	85	6.8	217	4	ABG16902	AbG16902 Novel hum
43	84.5	6.8	679	7	ADM05878	AdM05878 Human pro
44	84.5	6.8	679	7	ADN39904	Adn39904 Cancer/an
45	84	6.8	806	3	AA98055	Aa98055 Murine To

## ALIGNMENTS

RESULT 1	
AAB20089	standard; protein; 238 AA.
ID	AAB20089
AC	AAB20089;
XX	
DT	23-APR-2001 (first entry)
XX	
DE	Human hydrophobic domain-containing protein HP03303.
XX	
KW	Human; hydrophobic domain; antiinflammatory; immunosuppressive;
KW	immunostimulant; vulnerrary; antitumor; haemostatic; cytosolic;
KW	hepatotropic; thrombolytic; antitumor; antiviral; antibacterial;
KW	antifungal; gene therapy; diagnosis; membrane protein.
XX	
OS	Homo sapiens.
XX	
PH	Key
FT	Modified-site 29
XX	/note= "N-glycosylated"
XX	
PN	MO200100824-A2.
XX	
PD	04-JAN-2001.
XX	
PF	16-JUN-2000; 2000MO-JP003944.
XX	
PR	24-JUN-1999; 99JP-00178065.
XX	
PA	(SAGA ) SAGAMI CHEM RES CENT.
PA	(PROT-) PROTEGENE INC.
XX	
PI	Kato S, Kimura T;
XX	
DR	WPI; 2001-123008/13.
XX	
PT	N-PSDB; AAB20089.
XX	
PS	New protein with hydrophobic domains, useful for treating autoimmune
XX	diseases, inflammatory diseases, wounds, burns, incisions and ulcers.
XX	
CC	Claim 1; Page 85-86; 126pp; English.
CC	The present sequence is that of a novel human protein having an N-
CC	terminal transmembrane domain. It is predicted from cDNA clone HP03303
CC	(see AAF00207), isolated from a human liver cDNA library. The predicted
CC	protein shows sequence similarity to human hypocholesterol protein KIAA1007.
CC	The invention provides human proteins (see AAB20089-96) having
CC	hydrophobic domains indicative of secretory signals or membrane domains,

CC and nucleic acids (see AAF30020-27) encoding them. These are expected to  
 CC have cell proliferation, cell differentiation, immunostimulant or  
 CC immunosuppressor, haematopoiesis regulating, tissue growth, actinin,  
 CC inhibin, chemotactic, chemokinetic, haemostatic, thrombolytic,  
 CC receptor/ligand, antiinflammatory or antitumour activities (no evidence  
 CC provided). Expression vectors, eukaryotic host cells and antibodies are  
 CC also provided. The secreted or membrane proteins of the invention can be  
 CC used as pharmaceuticals or antigens for preparing antibodies. Cells  
 CC expressing them are utilized for detection of corresponding receptors or  
 CC ligands, and in candidate drug screening

XX Sequence 238 AA;

Query Match 100.0%; Score 1243; DB 4; Length 238;

Best Local Similarity 100.0%; Pred. No. 1.4e-131;

Matches 238; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MILLVTLAFYLMQVDMSEINIAPRILTNFTGVMPQPKDLDSYLKTRSPVTFSLDLRS 60  
 |||||  
 DB 1 MILLVTLAFYLMQVDMSEINIAPRILTNFTGVMPQPKDLDSYLKTRSPVTFSLDLRS 60  
 |||||  
 QY 61 NLOVSNBPGRRYMLQILNALVLYGTQALAHINKGSTPSMSTITTSAMDIFONTAVDL 120  
 |||||  
 DB 61 NLOVSNBPGRRYMLQILNALVLYGTQALAHINKGSTPSMSTITTSAMDIFONTAVDL 120  
 |||||  
 QY 121 DTGGRYLFPLNAIANOLRYPSNTHYFSCITMLYLPABANTBAIOEQITRVLLERLIYNRP 180  
 |||||  
 DB 121 DTGGRYLFPLNAIANOLRYPSNTHYFSCITMLYLPABANTBAIOEQITRVLLERLIYNRP 180  
 |||||  
 QY 181 PMGLITTFEILIKNPAPKFWNHEFVHCAPBEIKLFQSVACCMGQKQAQVMEGTGAS 238  
 |||||  
 DB 181 PMGLITTFEILIKNPAPKFWNHEFVHCAPBEIKLFQSVACCMGQKQAQVMEGTGAS 238  
 |||||

#### RESULT 2

ID ADQ96030 standard; protein; 638 AA.

XX ADQ96030;

DT 07-OCT-2004 (first entry)

DE T cell activation associated protein #104.

XX antiallergic; antiarthritic; antiasthmatic; antidiabetic; anti-HIV;  
 KM antimicrobial; antirheumatic; immunosuppressive; neuroprotective;  
 KM gene therapy; T cell activation; diagnosis; autoimmune disease;  
 KM rheumatoid arthritis; asthma; multiple sclerosis; diabetes;  
 KM allergic disease; infectious disease; AIDS; chronic rejection; organ;  
 KM bone-marrow transplant.

XX Homo sapiens.

PN WO2004058805-A2.

PD 15-JUL-2004.

PF 25-DEC-2003; 2003WO-JP016715.

PR 26-DEC-2002; 2002JP-00376365.

PR 27-DEC-2002; 2002US-0436473P.

PR 25-APR-2003; 2003JP-00122113.

PR 28-APR-2003; 2003US-0465792P.

PR 21-OCT-2003; 2003JP-00360559.

PR 22-OCT-2003; 2003US-0512846P.

XX (ASAH-) ASAMI KASEI PHARMA CORP.

XX Matsuuda A., Yoneta S;

PI WPI; 2004-583134/57.

DR N-PSDB; ADQ96029.

PT New purified protein involved in T cell activation, useful for  
 PT diagnosis, preventing and/or treating acquired immunodeficiency  
 PT syndrome, autoimmune (e.g. rheumatoid arthritis, and diabetes), allergic  
 PT and infectious diseases.

XX Claim 1; SEQ ID NO 208; 2828pp; English.

XX The invention relates to purified proteins and genes encoding them, that  
 CC are involved in T cell activation (I) and has an amino acid deletion,  
 CC substitution or addition in the amino acid sequences. The methods and  
 CC compositions of the present invention are useful for the diagnosis,  
 CC prevention and/or treatment of autoimmune disease (rheumatoid arthritis,  
 CC asthma, multiple sclerosis and diabetes), allergic disease, infectious  
 CC disease, AIDS, and acute or chronic rejection at organ transplant or bone  
 CC marrow transplant. This sequence corresponds to a protein involved in T  
 CC cell activation.

XX Sequence 638 AA;

Query Match 94.8%; Score 1178; DB 8; Length 638;

Best Local Similarity 99.6%; Pred. No. 1.4e-123;

Matches 225; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 13 QVDMSEINIAPRILTNFTGVMPQPKDLDSYLKTRSPVTFSLDLRSNLOVSNBPNRY 72  
 :|||  
 DB 413 QVDMSEINIAPRILTNFTGVMPQPKDLDSYLKTRSPVTFSLDLRSNLOVSNBPNRY 472  
 |||||  
 QY 73 NQILNALVLYGTQALAHINKGSTPSMSTITTSAMDIFONTAVDLDTGERYFLNAI 132  
 |||||  
 DB 473 NQILNALVLYGTQALAHINKGSTPSMSTITTSAMDIFONTAVDLDTGERYFLNAI 532  
 |||||  
 QY 133 ANOLRYPSNTHYFSCITMLYLPABANTBAIOEQITRVLLERLIYNRPMPGLITFIELI 192  
 |||||  
 DB 533 ANOLRYPSNTHYFSCITMLYLPABANTBAIOEQITRVLLERLIYNRPMPGLITFIELI 592  
 |||||  
 QY 193 KNPAKFWNHEFVHCAPBEIKLFQSVACCMGQKQAQVMEGTGAS 238  
 |||||  
 DB 593 KNPAKFWNHEFVHCAPBEIKLFQSVACCMGQKQAQVMEGTGAS 638  
 |||||

#### RESULT 3

ID ADQ96032 standard; protein; 638 AA.

XX ADQ96032;

DT 07-OCT-2004 (first entry)

DE T cell activation associated protein #105.

XX antiallergic; antiarthritic; antiasthmatic; antidiabetic; anti-HIV;  
 KM antimicrobial; antirheumatic; immunosuppressive; neuroprotective;  
 KM gene therapy; T cell activation; diagnosis; autoimmune disease;  
 KM rheumatoid arthritis; asthma; multiple sclerosis; diabetes;  
 KM allergic disease; infectious disease; AIDS; chronic rejection; organ;  
 KM bone-marrow transplant.

XX Homo sapiens.

PN WO2004058805-A2.

PD 15-JUL-2004.

PF 25-DEC-2003; 2003WO-JP016715.

PR 26-DEC-2002; 2002JP-00376365.

PR 27-DEC-2002; 2002US-0436473P.

PR 25-APR-2003; 2003JP-00122113.

PR 28-APR-2003; 2003US-0465792P.

PR 21-OCT-2003; 2003JP-00360559.

PR 22-OCT-2003; 2003US-0512846P.

XX (ASAH-) ASAMI KASEI PHARMA CORP.

XX Matbuda A, Yoneta S;  
PI WPI; 2004-593134/57.  
DR N-PSDB; ADA96031.  
XX  
PT New purified protein involved in T cell activation, useful for  
PT diagnosing, preventing and/or treating acquired immunodeficiency  
PT syndrome, autoimmune (e.g. rheumatoid arthritis, and diabetes), allergic  
PT and infectious diseases.  
XX  
PS Claim 1; SEQ ID NO 210; 2828bp; English.  
XX  
CC The invention relates to purified proteins and genes encoding them, that  
CC are involved in T cell activation (T) and has an amino acid deletion,  
CC substitution or addition in the amino acid sequences. The methods and  
CC compositions of the present invention are useful for the diagnosis,  
CC prevention and/or treatment of autoimmune disease (rheumatoid arthritis,  
CC asthma, multiple sclerosis and diabetes), allergic disease, infectious  
CC disease, AIDS, and acute or chronic rejection of organ transplant or bone  
CC marrow transplant. This sequence corresponds to a protein involved in T  
CC cell activation.  
XX  
SQ Sequence 638 AA;  
XX  
Query Match 94.8%; Score 1178; DB 8; Length 638;  
Best Local Similarity 99.6%; Pred. No. 1.4e-123;  
Matches 225; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
QY 13 QVDMLESLINAPRLINFTGVMPPQPKDLDSTLKTSPVTFSLDLSNQLVSNENPNRY 72  
:|||||  
DB 413 KVDMLSESLINAPRLINFTGVMPPQPKDLDSTLKTSPVTFSLDLSNQLVSNENPNRY 472  
QY 73 NLOLINALVLYVGTQAIHAIHNGKSTPSMSTTHSAMDIFQNLAVDLDTBGRYLFANAI 132  
DB 473 NLOLINALVLYVGTQAIHAIHNGKSTPSMSTTHSAMDIFQNLAVDLDTBGRYLFANAI 532  
QY 133 ANOLRYPNSTHTYFSCMTLYLPAEANTBAIOEITRVLERLIVNRHPWGLLITFIELI 192  
DB 533 ANOLRYPNSTHTYFSCMTLYLPAEANTBAIOEITRVLERLIVNRHPWGLLITFIELI 592  
QY 193 KNPAFKFKNHBFVHCAPETIKLFPQSVAAQCCMGKQKQAQWEGTAS 238  
DB 593 KNPAFKFKNHBFVHCAPETIKLFPQSVAAQCCMGKQKQAQWEGTAS 638  
XX  
RESULT 4  
ID ADA55285 standard; protein; 1070 AA.  
AC ADA55285;  
XX  
DT 20-NOV-2003 (first entry)  
XX  
DB Human protein, SEQ ID 2853.  
XX  
KM Cytostatic; Anti-inflammatory; Osteopathic; Neuroprotective; Nootropic;  
KM Gene therapy; human; secretory protein; membrane proteins; cancer;  
KM Inflammatory disease; osteoporosis; neurological disease.  
XX  
OS Homo sapiens.  
XX  
PN EP1293569-A2.  
XX  
PD 19-MAR-2003.  
XX  
PF 21-MAR-2002; 2002EP-00006586.  
XX  
PR 14-SEP-2001; 2001JP-00328381.  
XX  
PR 24-JAN-2002; 2002US-0350435P.  
XX  
PA (HELI-) HELIX RES INST.  
PA (REAS-) RES ASSOC BIOTECHNOLOGY.

XX Isegai T, Sugiyama T, Otsuki T, Wakamatsu A, Sato H, Iehli S;  
PI Yamamoto J, Isono Y, Hio Y, Otsuka K, Nagai K, Irie R, Tamechika I;  
PI Seki N, Yoshikawa T, Otsuka M, Nagahara K, Masuno Y;  
XX  
DR WPI; 2003-395539/38.  
DR N-PSDB; ADA53646.  
XX  
PT New polynucleotides encoding full-length polypeptides, e.g. secretory  
PT and/or membrane proteins, useful for developing medicines for diseases in  
PT which the gene is involved, or as target molecules for gene therapy.  
XX  
PS Claim 14; SEQ ID NO 2853; 2055bp; English.  
XX  
CC The present invention relates to novel human secretory or membrane  
CC proteins (ADA54072-ADA55710) and their coding sequences (ADA52433-  
CC ADA54071). The coding sequences are useful in the gene therapy of  
CC diseases caused by abnormalities of the proteins, e.g. cancer,  
CC inflammatory diseases, osteoporosis or neurological disease.  
XX  
SQ Sequence 1070 AA;  
XX  
Query Match 94.8%; Score 1178; DB 6; Length 1070;  
Best Local Similarity 99.6%; Pred. No. 3e-123;  
Matches 225; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
QY 13 QVDMLESLINAPRLINFTGVMPPQPKDLDSTLKTSPVTFSLDLSNQLVSNENPNRY 72  
:|||||  
DB 845 KVDMLSESLINAPRLINFTGVMPPQPKDLDSTLKTSPVTFSLDLSNQLVSNENPNRY 904  
QY 73 NLOLINALVLYVGTQAIHAIHNGKSTPSMSTTHSAMDIFQNLAVDLDTBGRYLFANAI 132  
DB 905 NLOLINALVLYVGTQAIHAIHNGKSTPSMSTTHSAMDIFQNLAVDLDTBGRYLFANAI 964  
QY 133 ANOLRYPNSTHTYFSCMTLYLPAEANTBAIOEITRVLERLIVNRHPWGLLITFIELI 192  
DB 965 ANOLRYPNSTHTYFSCMTLYLPAEANTBAIOEITRVLERLIVNRHPWGLLITFIELI 1024  
QY 193 KNPAFKFKNHBFVHCAPETIKLFPQSVAAQCCMGKQKQAQWEGTAS 238  
DB 1025 KNPAFKFKNHBFVHCAPETIKLFPQSVAAQCCMGKQKQAQWEGTAS 1070  
XX  
RESULT 5  
ID AAB43253 standard; protein; 1096 AA.  
AC AAB43253;  
XX  
DT 08-FEB-2001 (first entry)  
XX  
DE Human ORF3017 polypeptide sequence SEQ ID NO:6034.  
XX  
XX  
KM Human; open reading frame; ORF3; detection; cytostatic; hepatotropic;  
KM vulnerability; antiparkinsonian; nootropic; neuroprotective;  
KM anticonvulsant; osteopathic; antiarthritis; immunosuppressant; cardiac;  
KM immunostimulant; thrombolytic; coagulant; vasotropic; antidiabetic;  
KM hypotensive; dermatological; immunosuppressive; antiinflammatory;  
KM antiviral; antibacterial; antifungal; antirheumatic; antichryd;  
KM antianaemic; gene therapy; cancer; proliferative disorder; hypertension;  
KM neurodegenerative disorder; osteoarthritis; graft vs host disease;  
KM cardiovascular disease; diabetes mellitus; hypothyroidism; SCID; AIDS;  
KM cholesterol ester storage; systemic lupus erythematosus; infection;  
KM severe combined immunodeficiency; malaria; autoimmune disorder; asthma;  
KM allergy; aplastic anaemia; nocturnal haemoglobinuria; burn; wound;  
KM bone damage; cartilage damage; antiinflammatory disease; coagulation;  
KM thrombosis; contraceptive.  
XX  
OS Homo sapiens.  
XX  
PN WO200058473-A2.  
XX  
PD 05-OCT-2000.

```
XX 31-MAR-2000; 2000MO-US008621.
PF
XX 31-MAR-1999; 99US-0127607P.
PR
XX 02-APR-1999; 99US-0127636P.
PR
XX 05-APR-1999; 99US-0127728P.
PR
XX 30-MAR-2000; 2000US-00540763.
XX
XX (CURA-) CURAGEN CORP.
XX
XX Shinketsu RA, Leach M;
XX
XX MPI; 2000-602362/57.
XX
XX DR N-PSDB; AAC77462.
XX
XX PT Novel nucleic acids and peptides derived from open reading frame X,
XX neurodegenerative disorders and cardiovascular disease.
XX
XX PS Claim 11; Page 5218-5221; 5507pp; English.
XX
XX AAC74446 to AAC77606 encode the proteins given in AAB40237 to AAB43397,
XX which represent the human ORFX open reading frames 1 to 3161. The ORFX
XX sequences have activities such as: cytostatic; hepatotropic; vulnary;
XX antiparasitic; antiparkinsonian; nootropic; neuroprotective; osteopathic;
XX anticonvulsant; antiarthritic; immunosuppressant; immunostimulant;
XX cardiact; thrombolytic; coagulant; vasotropic; antidiabetic; hypotensive;
XX dermatological; immunosuppressive; antiinflammatory; antibacterial;
XX antiviral; antifungal; antirheumatic; antithyroid; and antianemic. The
XX sequences can be used for determining the presence of or predisposition
XX to, or preventing or treating pathological conditions associated with an
XX ORFX-associated disorder. The nucleic acids can be used to express ORFX
XX proteins in gene therapy vectors. The proteins and nucleic acids may be
XX used to treat cancer, proliferative disorders, neurodegenerative
XX disorders, osteoarthritis, graft vs host disease, cardiovascular disease,
XX diabetes mellitus, hypertension, hypothyroidism, cholesterol ester
XX storage, systemic lupus erythematosus, severe combined immunodeficiency
XX (SCID), AIDS, viral, bacterial or fungal infection, malaria, autoimmune
XX disorders, asthma, allergies, aplastic anemia, burns, wounds, bone and
XX cartilage damage, nocturnal haemoglobinuria, antiinflammatory disease; to
XX enhance coagulation; to inhibit thrombosis; and as a contraceptive
XX
XX SQ Sequence 1096 AA;
XX
XX Query Match 94.8%; Score 1178; DB 3; Length 1096;
XX Best Local Similarity 99.6%; Pred. No. 3.1e-123;
XX Matches 225; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 13 QVDMLESEINIAPIRLTNFTGVMPPOFKDLDLYLKTSPVTFSLDLSNMQVSNPGRNY 72
XX :|||||
XX DB 871 KYDMLSEINIAPIRLTNFTGVMPPOFKDLDLYLKTSPVTFSLDLSNMQVSNPGRNY 930
XX
XX QY 73 NQQLNALVLYVGTOAIAHIHNKGSTPSNSTTTHSAHMDIFONLAVDLDTBGRYFLNAI 132
XX :|||||
XX DB 931 NQQLNALVLYVGTOAIAHIHNKGSTPSNSTTTHSAHMDIFONLAVDLDTBGRYFLNAI 990
XX
XX QY 133 ANQLRPNSTHTYFSCITMLYFLAEANTEALQEQITRVLLERLIVNRPHPMGLITFIELI 192
XX :|||||
XX DB 991 ANQLRPNSTHTYFSCITMLYFLAEANTEALQEQITRVLLERLIVNRPHPMGLITFIELI 1050
XX
XX QY 193 KNPAFFMNHFEVHCAPETIEKLFQSVACCMGOKOAOQVMEGTGAS 238
XX :|||||
XX DB 1051 KNPAFFMNHFEVHCAPETIEKLFQSVACCMGOKOAOQVMEGTGAS 1096
XX
XX
XX RESULT 6
XX ADQ96036
XX ID ADQ96036 standard; protein; 1553 AA.
XX
XX AC ADQ96036;
XX
XX DT 07-OCT-2004 (first entry)
XX
```

```
DE T cell activation associated protein #107.
XX
XX anti-allergic; antiarthritic; antiasthmatic; antidiabetic; anti-HIV;
XX antimicrobial; antirheumatic; immunosuppressive; neuroprotective;
XX gene therapy; T cell activation; diagnosis; autoimmune disease;
XX rheumatoid arthritis; asthma; multiple sclerosis; diabetes;
XX allergic disease; infectious disease; AIDS; chronic rejection; organ;
XX bone-marrow transplant.
XX
XX OS Homo sapiens.
XX
XX PN WO2004058805-A2.
XX
XX PD 15-JUL-2004.
XX
XX PF 25-DEC-2003; 2003MO-JP016715.
XX
XX PR 26-DEC-2002; 2002JP-00376365.
XX
XX PR 27-DEC-2002; 2002US-0436473P.
XX
XX PR 25-APR-2003; 2003JP-00122113.
XX
XX PR 28-APR-2003; 2003US-0465792P.
XX
XX PR 21-OCT-2003; 2003JP-00360559.
XX
XX PR 22-OCT-2003; 2003US-0512846P.
XX
XX PA (ASAHI-) ASahi KASEI PHARMA CORP.
XX
XX PI Matsuda A, Yoneta S;
XX
XX DR MPI; 2004-593334/57.
XX
XX DR N-PSDB; ADQ96035.
XX
XX PT New purified protein involved in T cell activation, useful for
XX diagnosing, preventing and/or treating acquired immunodeficiency
XX syndrome, autoimmune (e.g. rheumatoid arthritis, and diabetes), allergic
XX and infectious diseases.
XX
XX PS Claim 1; SEQ ID NO 214; 2828pp; English.
XX
XX CC The invention relates to purified proteins and genes encoding them, that
XX are involved in T cell activation (1) and has an amino acid deletion,
XX substitution or addition in the amino acid sequences. The methods and
XX compositions of the present invention are useful for the diagnosis,
XX prevention and/or treatment of autoimmune disease (rheumatoid arthritis,
XX asthma, multiple sclerosis and diabetes), allergic disease, infectious
XX disease, AIDS, and acute or chronic rejection at organ transplant or bone
XX marrow transplant. This sequence corresponds to a protein involved in T
XX cell activation.
XX
XX SQ Sequence 1553 AA;
XX
XX Query Match 94.8%; Score 1178; DB 8; Length 1553;
XX Best Local Similarity 99.6%; Pred. No. 5.2e-123;
XX Matches 225; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 13 QVDMLESEINIAPIRLTNFTGVMPPOFKDLDLYLKTSPVTFSLDLSNMQVSNPGRNY 72
XX :|||||
XX DB 1328 KYDMLSEINIAPIRLTNFTGVMPPOFKDLDLYLKTSPVTFSLDLSNMQVSNPGRNY 1387
XX
XX QY 73 NQQLNALVLYVGTOAIAHIHNKGSTPSNSTTTHSAHMDIFONLAVDLDTBGRYFLNAI 132
XX :|||||
XX DB 1388 NQQLNALVLYVGTOAIAHIHNKGSTPSNSTTTHSAHMDIFONLAVDLDTBGRYFLNAI 1447
XX
XX QY 133 ANQLRPNSTHTYFSCITMLYFLAEANTEALQEQITRVLLERLIVNRPHPMGLITFIELI 192
XX :|||||
XX DB 1448 ANQLRPNSTHTYFSCITMLYFLAEANTEALQEQITRVLLERLIVNRPHPMGLITFIELI 1507
XX
XX QY 193 KNPAFFMNHFEVHCAPETIEKLFQSVACCMGOKOAOQVMEGTGAS 238
XX :|||||
XX DB 1508 KNPAFFMNHFEVHCAPETIEKLFQSVACCMGOKOAOQVMEGTGAS 1553
XX
XX
XX RESULT 7
XX AA02377
```

ID AAY02377 standard; protein; 1726 AA.  
 XX AAY02377;  
 AC  
 XX 13-JUL-1999 (first entry)  
 DT  
 XX  
 XX  
 DE Polypeptide identified by the signal sequence trap method.  
 KM Signal sequence trap method; SST method; immunisation; inhibition;  
 KM infection; allergy; cancer; regulation; tissue formation; tissue repair;  
 KM activin activity; inhibin activity; chemokine activity;  
 KM cytokine activity; blood coagulation regulation; agonist; antagonist;  
 KM metabolic disorder; hormonal disorder; immune disorder; wound;  
 KM severe combined immunodeficiency; SCID; AIDS; thrombosis; cancer.  
 XX Homo sapiens.  
 OS  
 XX WO918126-A1.  
 PN  
 XX 15-APR-1999.  
 PD  
 XX 06-OCT-1998; 98WO-JP004514.  
 PP  
 XX 07-OCT-1997; 97JP-00274674.  
 PR  
 XX (ONOV ) ONO PHARM CO LTD.  
 PA  
 XX Fukushima D, Shibayama S, Tada H;  
 PI  
 XX WPI; 1999-277254/23.  
 DR N-PSDB; AAX35732, AAX35733.  
 XX  
 PT Polypeptides identified by the signal sequence trap method from a human  
 PT cDNA library.  
 PT  
 XX Claim 1; Page 178-186; 281pp; Japanese.  
 XX  
 XX AA02358-84 represent novel polypeptides which are identified from a  
 CC human placental cDNA library by the signal sequence trap (SST) method.  
 CC The polypeptides are encoded by the cDNA sequences in AAX35694-X35747.  
 CC The polypeptides have a broad range of physiological activity, including  
 CC immunisation against and inhibition of infections, allergies and cancer;  
 CC regulation of tissue formation and repair; activin/inhibin activity;  
 CC chemokine/cytokine activity; blood coagulation regulation; and  
 CC receptor/ligand agonist or antagonist activity. The polypeptides can be  
 CC used for prevention and treatment of disorders including infections by  
 CC bacteria, yeasts and viruses (including HIV) and protozoa; metabolic and  
 CC hormonal disorders; immune disorders (including severe combined  
 CC immunodeficiency (SCID) and AIDS; thrombosis; cancer; and traumatic or  
 CC surgical wounds  
 CC  
 XX Sequence 1726 AA;  
 SQ  
 Query Match 94.8%; Score 1178; DB 2; Length 1726;  
 Best Local Similarity 99.6%; Pred. No. 6e-123;  
 Matches 225; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 13 QVDMLESRINAPRILNFTGVMPPQPKODLSYLTKRSPTVPLSDLSNLOVSNRPENRY 72  
 DB 1501 KVDMLSRINAPRILNFTGVMPPQPKODLSYLTKRSPTVPLSDLSNLOVSNRPENRY 1560  
 QY 73 NLOLINALVLYVGTQAIHAIHNKGSTPSNSTITHSAHMDIFQNLAVDLDTGGRYLFPLNAI 132  
 DB 1561 NLOLINALVLYVGTQAIHAIHNKGSTPSNSTITHSAHMDIFQNLAVDLDTGGRYLFPLNAI 1620  
 QY 133 ANOLRYNSHTHTFSCMTLYLPAEANTBAIOBQITRVLLRLIVNRPHPGGLITPTELI 192  
 DB 1621 ANOLRYNSHTHTFSCMTLYLPAEANTBAIOBQITRVLLRLIVNRPHPGGLITPTELI 1680  
 QY 193 KNPAFKFNHBFVHCAPRIEKLFGSVAAOCMGOKOAOVMEGTGAS 238  
 DB 1681 KNPAFKFNHBFVHCAPRIEKLFGSVAAOCMGOKOAOVMEGTGAS 1726

RESULT 8  
 ID ABB81196 standard; protein; 2141 AA.  
 XX ABB81196;  
 AC  
 XX 25-NOV-2002 (first entry)  
 DT  
 XX  
 XX  
 DE Human PNI3734 protein sequence.  
 KM SET; PNI2218; TTP; CIN85; PNI3734; TIAR; FUBP1; antiinflammatory;  
 KM antiarteriosclerotic; cardiatic; neurotropic; gene therapy; human.  
 XX  
 OS Homo sapiens.  
 XX  
 XX WO200264733-A2.  
 PN  
 XX 22-AUG-2002.  
 PD  
 XX 14-DEC-2001; 2001WO-US047655.  
 PP  
 XX 14-DEC-2000; 2000US-0255063P.  
 PR  
 XX (MYRI-) MYRIAD GENETICS INC.  
 PA  
 XX Cimborra DM, Heichman K, Bartel PL;  
 PI  
 XX WPI; 2002-643476/69.  
 DR N-PSDB; ABQ79531.  
 XX  
 PT New isolated protein complex comprising a first and second protein,  
 PT useful for the diagnosis and treatment of disorders involved in the  
 PT protein-protein interaction, such as inflammatory disease,  
 PT atherosclerosis or hypoxic brain injury.  
 PT  
 XX Claim 117; Page 23-24; 77pp; English.  
 XX  
 XX The invention relates to an isolated protein complex comprising 2  
 CC proteins. The protein complex comprises: (a) a first protein (P1) and a  
 CC second protein (P2); (b) a fragment P1 and P2; (c) P1 and a fragment P2;  
 CC and (d) a fragment of P1 and a fragment P2. The first and second proteins  
 CC of the complex are selected from: (1) P1 is SET, and P2 is PNI2218; (11)  
 CC P1 is TTP and P2 is CIN85 or PNI3734; or (111) P1 is TIAR and P2 is  
 CC FUBP1. The methods and compositions of the present invention are useful  
 CC for the diagnosis and/or treatment of physiological disorders involved in  
 CC the protein-protein interaction, such as inflammatory disease,  
 CC atherosclerosis, cardiac hypertrophy, or hypoxic brain injury. The drugs,  
 CC modulators, inhibitor or compounds are useful for treating the diseases  
 CC described above. The present sequence represents the predicted amino acid  
 CC sequence of PNI3734  
 CC  
 XX Sequence 2141 AA;  
 SQ  
 Query Match 94.8%; Score 1178; DB 5; Length 2141;  
 Best Local Similarity 99.6%; Pred. No. 8.3e-123;  
 Matches 225; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 13 QVDMLESRINAPRILNFTGVMPPQPKODLSYLTKRSPTVPLSDLSNLOVSNRPENRY 72  
 DB 1916 KVDMLSRINAPRILNFTGVMPPQPKODLSYLTKRSPTVPLSDLSNLOVSNRPENRY 1975  
 QY 73 NLOLINALVLYVGTQAIHAIHNKGSTPSNSTITHSAHMDIFQNLAVDLDTGGRYLFPLNAI 132  
 DB 1976 NLOLINALVLYVGTQAIHAIHNKGSTPSNSTITHSAHMDIFQNLAVDLDTGGRYLFPLNAI 2035  
 QY 133 ANOLRYNSHTHTFSCMTLYLPAEANTBAIOBQITRVLLRLIVNRPHPGGLITPTELI 192  
 DB 2036 ANOLRYNSHTHTFSCMTLYLPAEANTBAIOBQITRVLLRLIVNRPHPGGLITPTELI 2095  
 QY 193 KNPAFKFNHBFVHCAPRIEKLFGSVAAOCMGOKOAOVMEGTGAS 238  
 DB 2096 KNPAFKFNHBFVHCAPRIEKLFGSVAAOCMGOKOAOVMEGTGAS 2141

```

RESULT 9
ID ABR58313
ID ABR58313 standard; protein; 2376 AA.
AC ABR58313;
DT 08-JUL-2003 (first entry)
DE BC00586 protein #SEQ ID 72.
KW Breast cancer; cytostatic; gene therapy; antisense therapy; regulated;
KW drug discovery; clinical medicine; forensic medicine; chromosome 16q13.
OS Homo sapiens.
PN WO2003029421-A2.
PN 10-APR-2003.
PD 02-OCT-2002; 2002WO-US031287.
PR 03-OCT-2001; 2001US-0326526P.
PR 14-MAY-2002; 2002US-00144194.
XX (ORIG-) ORIGENE TECHNOLOGIES INC.
XX Sun Z, Li X, Fan W, Kovacs KF, Jay G;
PI WPI; 2003-381623/36.
DR N-PSDB; ACC72047.
XX
XX New isolated human differentially-regulated breast cancer polynucleotide
PT and polypeptide, useful for diagnosing, staging, prognosticating,
PT preventing and/or treating diseases and conditions relating to breast
PT cancer.
XX
XX Claim 6; SEQ ID NO 72; 127pp + Sequence listing; English.
XX
XX The invention relates to isolated polynucleotides which are
XX differentially-regulated in breast cancer. The methods and compositions
XX of the present invention are useful for detecting, diagnosing, staging,
XX monitoring, prognosticating, preventing and/or treating diseases and
XX conditions relating to breast cancer, and may be used in gene therapy or
XX antisense therapy. They can also be used in research, drug discovery,
XX clinical medicine and forensic medicine. Sequences given in records
XX CC ABR58278-ABR58323 and ABR58346-ABR58362 represent polypeptides encoded by
XX polynucleotides of the invention that are differentially-regulated in
XX breast cancer. NOTE: The sequence data for this patent did not form part
XX of the printed specification, but was obtained in electronic format
XX directly from WIPO at ftp.wipo.int/pub/published_pcc_sequences
XX
XX Sequence 2376 AA;
SQ
XX
XX Query Match          94.8%; Score 1178; DB 6; Length 2376;
XX Best Local Similarity 99.6%; Pred. No. 9.7e-123;
XX Matches 225; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
XX
XX 13 QVDMLESEINIAPIRLTNFTGVPMPQPKDLSYLTSTRSPVTLSDLRSLQVSNBGRNY 72
XX :|||||
XX 2151 KVDMLSEINIAPIRLTNFTGVPMPQPKDLSYLTSTRSPVTLSDLRSLQVSNBGRNY 2210
XX
XX 73 NQOLINALVLYGTQAIHAIHNKGSTPSNSTITTHSAHMDIFQNLAVDLDTBGRYLFINAI 132
XX :|||||
XX 2211 NQOLINALVLYGTQAIHAIHNKGSTPSNSTITTHSAHMDIFQNLAVDLDTBGRYLFINAI 2270
XX
XX 133 ANOLRPNSHTHFTSCMTLYLPAEANTBAIOEITVLLERLIVNRPHPMGLITFIELI 192
XX :|||||
XX 2271 ANOLRPNSHTHFTSCMTLYLPAEANTBAIOEITVLLERLIVNRPHPMGLITFIELI 2330
XX
XX 193 KNPAKFMNHEFVHCAPETIEKLFOQVAQCCMGOKOAOQWEGTGAS 238
XX :|||||
XX

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DB 2331 KNPAKFMNHEFVHCAPETIEKLFOQVAQCCMGOKOAOQWEGTGAS 2376
XX
XX RESULT 10
XX ADQ96034
XX ID ADQ96034 standard; protein; 2376 AA.
XX
XX ADQ96034;
XX
XX 07-OCT-2004 (first entry)
XX
XX T cell activation associated protein #106.
XX
XX antiallergic; antiarthritic; antiasthmatic; antidiabetic; anti-HIV;
XX antimicrobial; antirheumatic; immunosuppressive; neuroprotective;
XX gene therapy; T cell activation; diagnosis; autoimmune disease;
XX rheumatoid arthritis; asthma; multiple sclerosis; diabetes;
XX allergic disease; infectious disease; AIDS; chronic rejection; organ;
XX bone-marrow transplant.
XX
XX Homo sapiens.
XX
XX WO2004058805-A2.
XX
XX 15-JUL-2004.
XX
XX 25-DEC-2003; 2003WO-JP016715.
XX
XX 26-DEC-2002; 2002JP-00376365.
XX 27-DEC-2002; 2002US-0436473P.
XX 25-APR-2003; 2003JP-00122113.
XX 28-APR-2003; 2003US-0465792P.
XX 21-OCT-2003; 2003JP-00360559.
XX 22-OCT-2003; 2003US-0512846P.
XX
XX (ASAHI-) ASAHI KASEI PHARMA CORP.
XX
XX Matsuda A, Yoneta S;
XX
XX WPI; 2004-593134/57.
XX N-PSDB; ADQ96033.
XX
XX New purified protein involved in T cell activation, useful for
XX diagnosing, preventing and/or treating acquired immunodeficiency
XX syndrome, autoimmune (e.g. rheumatoid arthritis, and diabetes), allergic
XX and infectious diseases.
XX
XX Claim 1; SEQ ID NO 212; 2828pp; English.
XX
XX The invention relates to purified proteins and genes encoding them, that
XX are involved in T cell activation (I) and has an amino acid deletion,
XX substitution or addition in the amino acid sequences. The methods and
XX compositions of the present invention are useful for the diagnosis,
XX prevention and/or treatment of autoimmune disease (rheumatoid arthritis,
XX asthma, multiple sclerosis and diabetes), allergic disease, infectious
XX disease, AIDS, and acute or chronic rejection at organ transplant or bone
XX -marrow transplant. This sequence corresponds to a protein involved in T
XX cell activation.
XX
XX Sequence 2376 AA;
SQ
XX
XX Query Match          94.8%; Score 1178; DB 8; Length 2376;
XX Best Local Similarity 99.6%; Pred. No. 9.7e-123;
XX Matches 225; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
XX
XX 13 QVDMLESEINIAPIRLTNFTGVPMPQPKDLSYLTSTRSPVTLSDLRSLQVSNBGRNY 72
XX :|||||
XX 2151 KVDMLSEINIAPIRLTNFTGVPMPQPKDLSYLTSTRSPVTLSDLRSLQVSNBGRNY 2210
XX
XX 73 NQOLINALVLYGTQAIHAIHNKGSTPSNSTITTHSAHMDIFQNLAVDLDTBGRYLFINAI 132
XX :|||||
XX 2211 NQOLINALVLYGTQAIHAIHNKGSTPSNSTITTHSAHMDIFQNLAVDLDTBGRYLFINAI 2270
XX

```

QY 133 ANQLRPNSTHTYFSCMTLYLPABANTBAIOEOTITRVLLERLIYNRPHPGLITITIELI 192  
 |||||  
 DB 2271 ANQLRPNSTHTYFSCMTLYLPABANTBAIOEOTITRVLLERLIYNRPHPGLITITIELI 2330  
 |||||  
 QY 193 KNPAFKFMNHEFVHCAPBEIKLFGSVVACCCMGOKOAOQVNEGTSAS 238  
 |||||  
 DB 2331 KNPAFKFMNHEFVHCAPBEIKLFGSVVACCCMGOKOAOQVNEGTSAS 2376  
 |||||

## RESULT 11

ADQ08792  
 ID ADQ08792 standard; protein; 1167 AA.

AC ADQ08792;

DT 26-AUG-2004 (first entry)

DE Ciona intestinalis nervous system associated protein SegID:194.

XX gene cluster; nervous system; sea-squirt tailbud; embryo; larva;

KW nervous system disease.

OS Ciona intestinalis.

PN JP2004057127-A.

PD 26-FEB-2004.

PF 31-JUL-2002; 2002JP-00222532.

PR 31-JUL-2002; 2002JP-00222532.

PA (KAGA-) KAGAKU GIUTTSU SHINKO JIGYODAN.

DR WPI; 2004-208712/20.

DR N-PSDB; ADQ08791.

PT Novel genes derived from Ciona intestinalis (sea squirt), expressed in  
 PT nervous system in the tailbud embryo or larva, useful for studying the  
 PT development of nervous system.

PS Claim 4; SEQ ID NO 194; 897pp; Japanese.

CC This invention relates to a novel gene cluster, where the encoded  
 CC proteins are expressed in the nervous system of sea-squirt tailbud embryo  
 CC or larva. The invention is useful for studying the development of the  
 CC nervous system of the sea-squirt and for research purposes. The genes may  
 CC be used for determining the disease-development mechanisms in the nervous  
 CC system. In addition, novel gene clusters expressed in nervous system of  
 CC sea-squirt tailbud embryo or larva allows development of diagnostics and  
 CC therapeutics related to nervous system diseases. The present sequence is  
 CC that of a protein encoded by a C intestinalis gene of the invention.

XX Sequence 1167 AA;

XX Query Match 79.1%; Score 983; DB 8; Length 1167;

XX Best Local Similarity 81.4%; Pred. No. 3.8e-101;

XX Matches 184; Conservative 22; Mismatches 20; Indels 0; Gaps 0;

QY 13 OVDMLSEINAPRIILNFGVMPPOFKDLSYLTSTRSPVTFSLDSRNLQVSNBGNRY 72  
 |||||

DB 931 KVDMLSEINAPRIILNFGVMPPOFKDLSYLTSTRSPVTFSLDSRNLQVSNBGNRY 990  
 |||||

QY 73 NGLINLVLYVGTQIAIHINKGSTPSMSTITHSAHMDIFQNLAVDLDTGRYLPANAI 132  
 |||||

DB 991 NVELINSLVHVGTOIAIYIHNKGSPTSMTITHSHMDIFQNLAVDLDTGRYLPANAI 1050  
 |||||

QY 133 ANQLRPNSTHTYFSCMTLYLPABANTBAIOEOTITRVLLERLIYNRPHPGLITITIELI 192  
 |||||

DB 1051 ANQLRPNSTHTYFSCMTLYLPABANTBAIOEOTITRVLLERLIYNRPHPGLITITIELI 1110  
 |||||

QY 193 KNPAFKFMNHEFVHCAPBEIKLFGSVVACCCMGOKOAOQVNEGTSAS 238  
 |||||

DB 1111 KNPAFKFMNHEFVHCAPBEIKLFGSVVACCCMGOKOAOQVNEGTSAS 1156  
 |||||

## RESULT 12

ABG04093  
 ID ABG04093 standard; protein; 354 AA.

AC ABG04093;

DT 13-FEB-2002 (first entry)

DE Novel human diagnostic protein #4084.

XX human; chromosome mapping; gene mapping; gene therapy; forensic;

KW food supplement; medical imaging; diagnostic; genetic disorder.

OS Homo sapiens.

PN W0200175067-A2.

PD 11-OCT-2001.

PF 30-MAR-2001; 2001WO-US008631.

PR 31-MAR-2000; 2000US-00540217.

PR 23-AUG-2000; 2000US-00649167.

PA (HYSB-) HYSB INC.

PI Dmanac RT, Liu C, Tang YT;

DR WPI; 2001-639362/73.

DR N-PSDB; AAS68280.

PT New isolated polynucleotide and encoded polypeptide, useful in  
 PT diagnostics, forensics, gene mapping, identification of mutations  
 PT responsible for genetic disorders or other traits and to assess  
 PT biodiversity.

PS Claim 20; SEQ ID NO 34452; 103pp; English.

CC The invention relates to isolated polynucleotide (I) and polypeptide (II)  
 CC sequences. (I) is useful as hybridisation probes, polymerase chain  
 CC reaction (PCR) primers, oligomers, and for chromosome and gene mapping,  
 CC and in recombinant production of (II). The polynucleotides are also used  
 CC in diagnostics as expressed sequence tags for identifying expressed  
 CC genes. (I) is useful in gene therapy techniques to restore normal  
 CC activity of (II) or to treat disease states involving (II). (II) is  
 CC useful for generating antibodies against it, detecting or quantitating a  
 CC polypeptide in tissue, as molecular weight markers and as a food  
 CC supplement. (II) and its binding partners are useful in medical imaging  
 CC of sites expressing (II). (I) and (II) are useful for treating disorders  
 CC involving aberrant protein expression or biological activity. The  
 CC polypeptide and polynucleotide sequences have applications in  
 CC diagnostics, forensics, gene mapping, identification of mutations  
 CC responsible for genetic disorders or other traits to assess biodiversity  
 CC and to produce other types of data and products dependent on DNA and  
 CC amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic  
 CC amino acid sequences of the invention. Note: The sequence data for this  
 CC patent did not appear in the printed specification, but was obtained in  
 CC electronic format directly from WIPO at  
 CC ftp://ipoint/pub/published\_pat\_sequences

XX Sequence 354 AA;

XX Query Match 79.0%; Score 982; DB 4; Length 354;

XX Best Local Similarity 95.5%; Pred. No. 8.4e-102;

XX Matches 190; Conservative 2; Mismatches 5; Indels 2; Gaps 2;

QY 13 OVDMLSEINAPRIILNFGVMPPOFKDLSYLTSTRSPVTFSLDSRNLQVSNBGNRY 72  
 |||||

DB 156 KVDMLSEINAPRIILNFGVMPPOFKDLSYLTSTRSPVTFSLDSRNLQVSNBGNRY 215  
 |||||



QY 73 NIQLINALVLYGTOALIAIHKKSGSPSMSTTHSHAMDI FQNLAVDLDTGKRYLPLNAI 132

Db 216 NIQLINALVLYGTOALIAIHKKSGSPSMSTTHSHAMDI FQNLAVDLDTGKRYLPLNAI 275

QY 133 ANQLAPNSHTHYFSCSTMLYLPA -EANT -EALQEQITRVILLELIVNRPHPMGLITTFIE 150

Db 276 ANQLAPNSHTHYFSCSTMLYLPGRRANSGRPFQBOQITRVILLELIVNRPHPMGLITTFIE 335

QY 191 LIKNPAKFMNHEFYHCAP 209

Db 336 LIKNPAKFMNHEFYHCAP 354

RESULT 13  
AAM93552  
ID AAM93552 standard; protein; 873 AA.

AC	AAM93552;
XX	
DT	06-NOV-2001 (first entry)
XX	
DE	Human polypeptide, SEQ ID NO: 3315.
KW	Human; full length cDNA; cDNA synthesis; oligo-capping.
XX	
OS	Homo sapiens.
XX	
PN	EP1130094-A2.
XX	
PD	05-SEP-2001.
XX	
PF	07-JUL-2000; 2000EP-00114089.
XX	
PR	08-JUL-1999; 99JP-00194486.
PR	11-MAY-2000; 2000JP-00118774.
PR	02-MAY-2000; 2000JP-00183765.
XX	
PA	(HELI-) HELIX RES INST.
Pt	Ota T, Nishikawa T, Iyoga T, Hayaishi K, Ishii S, Kawai Y;
Pt	Makematsu A, Sugiyama T, Nagai K, Kojima S, Otsuki T, Koga H;
XX	
DR	WPI; 2001-524255/58.
DR	N-FSDB; AAK94484.
XX	
Pt	830 Primers useful for synthesizing full length cDNA clones and their use
Pt	in genetic manipulation.
XX	
PS	Claim 8; SEQ ID NO 3315; 1380pp + Sequence Listing; English.
XX	
CC	The invention relates to primers for synthesizing full length cDNA
CC	clones. 830 cDNA molecules encoding a human protein have been isolated
CC	and nucleotide sequences of 5'- and 3'-ends of the cDNA molecules have
CC	been determined. Primers for synthesizing the full length cDNA are useful
CC	for clarifying the function of the protein encoded by the cDNA. The full
CC	length clones were obtained by construction of full length enriched cDNA
CC	libraries that were synthesized by the oligo-capping method. The primers
CC	enable the production of the full length cDNA easily without any special
CC	methods. The present sequence is a polypeptide encoded by a full length
CC	human cDNA of the invention. Note: The sequence data for this patent did
CC	not form part of the printed specification, but was obtained in CD-ROM
CC	format directly from EPO
XX	
SQ	Sequence 873 AA;

Very Match	76.5%	Score 951;	DB 4;	Length 873;
Net Local Similarity	99.5%;	Pred. No. 1e-97;		
Matches 184; Conservative	1;	Mismatches	0;	Indels 0; Gaps 0

QY 13 QVDMSEINIA<sup>1</sup>PRILNFTGWP<sup>2</sup>PO<sup>3</sup>KKOLD<sup>4</sup>SYL<sup>5</sup>KT<sup>6</sup>SPV<sup>7</sup>TLSD<sup>8</sup>LA<sup>9</sup>SN<sup>10</sup>LO<sup>11</sup>YS<sup>12</sup>NE<sup>13</sup>PG<sup>14</sup>RY 72

Db 689 KADMSEINIA<sup>1</sup>PRILNFTGWP<sup>2</sup>PO<sup>3</sup>KKOLD<sup>4</sup>SYL<sup>5</sup>KT<sup>6</sup>SPV<sup>7</sup>TLSD<sup>8</sup>LA<sup>9</sup>SN<sup>10</sup>LO<sup>11</sup>YS<sup>12</sup>NE<sup>13</sup>PG<sup>14</sup>RY 748

Qy	73	NQQLINALVLYVGTQALIAIHNRKSGTSPGSGSTITHSAHMDIFQNLAVLDTEGRLFTINAI	1323
Db	749	NQLINALVLYVGTQALIAIHNRKSGTSPGSGSTITHSAHMDIFQNLAVLDTEGRLFTINAI	808
Qy	133	ANQLRYPNSHTHYFSGTMYLFAEAANTEALQOQITRVLLERLIYNRPHPGMLITFTIELI	1926
Db	809	ANQLRYPNSHTHYFSGTMYLFAEAANTEALQOQITRVLLERLIYNRPHPGMLITFTIELI	866
Qy	193	KNPAF 197	
Db	869	KNPAF 873	

RESULT 14  
ADL31282  
ID ADL31282 standard; protein; 873 AA

AC ADL31282;  
XX  
XX 20-MAY-2004 (first entry)  
DT  
XX Human protein encoded by a full length cDNA clone SegID 3315.  
DE  
XX human; medicine; signal transduction; glycoprotein; transcription;  
KW oligo-capping method.  
XX  
XX Homo sapiens.  
OS  
XX EPI396543-A2.  
PN  
XX 10-MAR-2004.  
PD  
XX  
XX 07-JUL-2000; 2003EP-00025638.  
PF  
XX  
XX 08-JUL-1999; 99JP-00194486.  
PR 11-JAN-2000; 2000JP-00118774.  
PR 02-MAY-2000; 2000JP-00183865.  
PR 07-JUL-2000; 2000EP-00114089.  
XX  
XX  
PA (REAS-) RES ASSOC BIOTECHNOLOGY.  
XX  
XX Ota T, Nishikawa T, Isogai T, Hayashi K, Ishii S, Kawai Y;  
PI Wakamatsu A, Sugiyama T, Nagai K, Kojima S, Otsuki T, Koga H;  
PI WPI; 2004-204755/20.  
DR  
XX N-PSDB; ADL31281.  
XX  
XX New oligonucleotide primers (830 cDNAs) useful for synthesizing full  
PT length human cDNAs.  
XX  
XX Example 1; SEQ ID NO 3315; 1340bp; English.  
PS  
XX  
XX This invention relates to a novel primers useful for synthesizing full  
CC length cDNA molecules that encode human proteins. Specifically, it refers  
CC to secretory or membrane proteins that are potential therapeutic agents/  
CC target molecules in the field of medicine, and in particular genes  
CC encoding proteins that are associated with signal transduction.  
CC glycoproteins and transcription. The present invention describes a method  
CC for efficiently cloning a full length human cDNA from both the 5' and 3'  
CC ends using the oligo-capping method. This polypeptide sequence is a full  
CC length human protein of the invention.

**SQ** Sequence 873 AA;

Query Match	76.5%	Score 951	DB 8	Length 873
Best Local Similarity	99.5%	Pred. No. 1e-97		
Matches 184	Conservative 1	Mismatches 0	Indels 0	Gaps 0

Db 689 KVDMLSEINAPRIITNFTGVMPPQEKDLSYLTKTRSPVTFLLSDLRSLQVSNPEGRKY 748



```

Db      749  |||||
Qy      133  ANQLRYNSHTHYFSCMTLYIPAEANTEAIOEQITVLERLIVNRPHPGLLITPIELI
Db      809  ANQLRYNSHTHYFSCMTLYIPAEANTEAIOEQITVLERLIVNRPHPGLLITPIELI
Qy      193  KNPAF 197
Db      869  KNPAF 873

```

## RESULT 15

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ABB58631
ID  ABB58631 standard; protein; 1766 AA.
XX
AC  ABB58631;
XX
DT  26-MAR-2002 (first entry)
XX
DE  Drosophila melanogaster polypeptide SEQ ID NO 2685.
XX
KM  Drosophila; developmental biology; cell signalling; insecticide;
XX  pharmaceutical.
XX
OS  Drosophila melanogaster.
XX
PN  NC0200171042-A2.
XX
PD  27-SEP-2001.
XX
PF  23-MAR-2001; 2001MO-US009231.
XX
PR  23-MAR-2000; 2000US-0191637P.
XX  11-JUL-2000; 2000US-00614150.
XX
PA  (PEKE ) PE CORP NY.
XX
PI  Venter JC, Adams M, Li FWD, Myers EW;
XX  WPI; 2001-656860/75.
XX  N-PSDB; ABL02734.
XX
PT  New isolated nucleic acid detection reagent for detecting 1000 or more
XX  genes from Drosophila and for elucidating cell signalling and cell-cell
XX  interactions.
XX
PS  Disclosure; SEQ ID NO 2685; 21pp + Sequence listing; English.
XX
CC  The invention relates to an isolated nucleic acid detection reagent
XX  capable of detecting 1000 or more genes from Drosophila. The invention is
XX  useful in developmental biology and in elucidating cell signalling and
XX  cell-cell interactions in higher eukaryotes for the development of
XX  insecticides, therapeutic and pharmaceutical drugs. The invention
XX  discloses genomic DNA sequences (AB116176-AB130511), expressed DNA
XX  sequences (AB101840-AB116175) and the encoded proteins (ABB57737-
XX  ABB72072). The sequence data for this patent did not form part of the
XX  printed specification, but was obtained in electronic format directly
XX  from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
SQ  Sequence 1766 AA;

```

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Query Match      70.2%; Score 873; DB 4; Length 1766;
Best Local Similarity 71.7%; Pred. No. 2e-88;
Matches 165; Conservative 30; Mismatches 29; Indels 6; Gaps 2;

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Qy      13  QVDMLSRINTAPRLTNP-TGVMPQPKQLDSYLTGRSPVTFISDLSRNLQVSNBERGR 71
Db      1530  KVMKLDSSNAKPKLSSYINQIPANKKQLDSTLKKAPVTFLSKRGHLQVTSRPGTR 1589
Qy      72  YNLQILNALVLYVGTQALIAHINHGSTPSMTTTHSAMDI PONTAVDLDTGGRYLFINA 131
Db      1590  YNMAIMNALVMYVGTQALIRKKNFVPNTSNIAHSAMDIPONTAVDLDTGGRYLFINA 1649

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Qy      132  IANQLRYNSHTHYFSCMTLYIPAEANTEAIOEQITVLERLIVNRPHPGLLITPIEL 191
Db      1650  IANQLRYNSHTHYFSCAVLHLFAEANSBAIOEQITVLERLIVNRPHPGLLITPIEL 1709
Qy      192  IKNPAPKFMNHEFVHCAPSEIEKLFGSVAGCCMGQKAAQ-----VMEGTG 236
Db      1710  IKNPITYKFMHDVHCAPSEITKLFGSVARSCIAKSNVTQQLNMPVVDGEG 1759

```

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Search completed: July 14, 2005, 20:27:10
Job time : 84.9612 secs

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LENGTH: 1070  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-094-749-2853

Query Match 94.8%; Score 1178; DB 15; Length 1070;  
Best Local Similarity 99.6%; Pred. No. 1.1e-116;  
Matches 225; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

13 QVDMLEINIAPIRLNFTGVMPPOFKDLSYKTRSPVTFSLDRSNLQVNEPGNRY 72  
:|||||  
845 KQDMLSEINIAPIRLNFTGVMPPOFKDLSYKTRSPVTFSLDRSNLQVNEPGNRY 904  
|||  
73 NQOLINALVLYGTQAIHAIHNKGSTPSMSTITTHSAHMDIFQNLAVDLDTGRYLFPLNAI 132  
|||||  
905 NQOLINALVLYGTQAIHAIHNKGSTPSMSTITTHSAHMDIFQNLAVDLDTGRYLFPLNAI 964  
|||||  
133 ANGLRYPNSHTYFSCMTLYLPABANTBAIOEQITRVLLERLIIVNRPHPWGLLITFIELI 192  
|||||  
965 ANGLRYPNSHTYFSCMTLYLPABANTBAIOEQITRVLLERLIIVNRPHPWGLLITFIELI 1024  
|||||  
193 KNPAKFMNHEFVHCAPETIKLFGSVAQCCMGQKQAQVMEGTGAS 238  
|||||  
1025 KNPAKFMNHEFVHCAPETIKLFGSVAQCCMGQKQAQVMEGTGAS 1070  
|||||

RESULT 2  
US-09-529-063-58  
Sequence 58, Application US/09529063  
Patent No. US20020102542A1  
GENERAL INFORMATION:  
APPLICANT: FUKUSHIMA, DAICHI  
APPLICANT: SHIBAYAMA, SHIRO  
APPLICANT: TADA, HIDEAKI  
TITLE OF INVENTION: POLYPEPTIDE, CDNA ENCODING THE POLYPEPTIDE, AND USE OF  
FILE REFERENCE: 058769  
CURRENT APPLICATION NUMBER: US/09/529,063  
PRIOR FILING DATE: 2000-04-07  
PRIOR APPLICATION NUMBER: PCT/JP98/04514  
PRIOR FILING DATE: 1998-10-06  
PRIOR APPLICATION NUMBER: JP 9-274674  
PRIOR FILING DATE: 1997-10-07  
NUMBER OF SEQ ID NOS: 117  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 58  
LENGTH: 1726  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-529-063-58

Query Match 94.8%; Score 1178; DB 9; Length 1726;  
Best Local Similarity 99.6%; Pred. No. 2.2e-116;  
Matches 225; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

13 QVDMLEINIAPIRLNFTGVMPPOFKDLSYKTRSPVTFSLDRSNLQVNEPGNRY 72  
:|||||  
1501 KQDMLSEINIAPIRLNFTGVMPPOFKDLSYKTRSPVTFSLDRSNLQVNEPGNRY 1560  
|||  
73 NQOLINALVLYGTQAIHAIHNKGSTPSMSTITTHSAHMDIFQNLAVDLDTGRYLFPLNAI 132  
|||||  
1561 NQOLINALVLYGTQAIHAIHNKGSTPSMSTITTHSAHMDIFQNLAVDLDTGRYLFPLNAI 1620  
|||||  
133 ANGLRYPNSHTYFSCMTLYLPABANTBAIOEQITRVLLERLIIVNRPHPWGLLITFIELI 192  
|||||  
1621 ANGLRYPNSHTYFSCMTLYLPABANTBAIOEQITRVLLERLIIVNRPHPWGLLITFIELI 1680  
|||||  
193 KNPAKFMNHEFVHCAPETIKLFGSVAQCCMGQKQAQVMEGTGAS 238  
|||||  
1681 KNPAKFMNHEFVHCAPETIKLFGSVAQCCMGQKQAQVMEGTGAS 1726  
|||||

RESULT 3

US-10-414-378-58  
Sequence 58, Application US/10414378  
Publication No. US20030016598A1  
GENERAL INFORMATION:  
APPLICANT: FUKUSHIMA, DAICHI  
APPLICANT: SHIBAYAMA, SHIRO  
APPLICANT: TADA, HIDEAKI  
TITLE OF INVENTION: POLYPEPTIDE, CDNA ENCODING THE POLYPEPTIDE, AND USE OF  
FILE REFERENCE: 058769  
CURRENT APPLICATION NUMBER: US/10/414,378  
PRIOR FILING DATE: 2003-04-16  
PRIOR APPLICATION NUMBER: US/09/529,063  
PRIOR FILING DATE: 2000-04-07  
PRIOR APPLICATION NUMBER: PCT/JP98/04514  
PRIOR FILING DATE: 1998-10-06  
PRIOR APPLICATION NUMBER: JP 9-274674  
PRIOR FILING DATE: 1997-10-07  
NUMBER OF SEQ ID NOS: 117  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 58  
LENGTH: 1726  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-414-378-58

Query Match 94.8%; Score 1178; DB 14; Length 1726;  
Best Local Similarity 99.6%; Pred. No. 2.2e-116;  
Matches 225; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

13 QVDMLEINIAPIRLNFTGVMPPOFKDLSYKTRSPVTFSLDRSNLQVNEPGNRY 72  
:|||||  
1501 KQDMLSEINIAPIRLNFTGVMPPOFKDLSYKTRSPVTFSLDRSNLQVNEPGNRY 1560  
|||  
73 NQOLINALVLYGTQAIHAIHNKGSTPSMSTITTHSAHMDIFQNLAVDLDTGRYLFPLNAI 132  
|||||  
1561 NQOLINALVLYGTQAIHAIHNKGSTPSMSTITTHSAHMDIFQNLAVDLDTGRYLFPLNAI 1620  
|||||  
133 ANGLRYPNSHTYFSCMTLYLPABANTBAIOEQITRVLLERLIIVNRPHPWGLLITFIELI 192  
|||||  
1621 ANGLRYPNSHTYFSCMTLYLPABANTBAIOEQITRVLLERLIIVNRPHPWGLLITFIELI 1680  
|||||  
193 KNPAKFMNHEFVHCAPETIKLFGSVAQCCMGQKQAQVMEGTGAS 238  
|||||  
1681 KNPAKFMNHEFVHCAPETIKLFGSVAQCCMGQKQAQVMEGTGAS 1726  
|||||

RESULT 4  
US-10-014-814-6  
Sequence 6, Application US/10014814  
Publication No. US20030032058A1  
GENERAL INFORMATION:  
APPLICANT: Myriad Genetics, Inc.  
APPLICANT: Cimbora, Daniel M.  
APPLICANT: Heichman, Karen  
APPLICANT: Bartel, Paul L.  
TITLE OF INVENTION: Protein-Protein Interactions  
FILE REFERENCE: 2318-277-II  
CURRENT APPLICATION NUMBER: US/10/014,814  
PRIOR FILING DATE: 2001-12-14  
PRIOR APPLICATION NUMBER: US 60/255,063  
PRIOR FILING DATE: 2000-12-14  
NUMBER OF SEQ ID NOS: 6  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 6  
LENGTH: 2141  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-014-814-6

Query Match 94.8%; Score 1178; DB 14; Length 2141;  
Best Local Similarity 99.6%; Pred. No. 3e-116;  
Matches 225; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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QY 13 QVDMLESEINIAPIRLTNFTGVMPPQFKDLSYLTXTSPVTFSLDLSNLOVSNBGNRY 72
:|||||
DB 1916 KVMLESEINIAPIRLTNFTGVMPPQFKDLSYLTXTSPVTFSLDLSNLOVSNBGNRY 1975
QY 73 NQOLINALVLYVGTQAIHAHINKGSTPSMSTITHSAHMDIFONLAVDLDTBGRYLFPLNAI 132
|||||
DB 1976 NQOLINALVLYVGTQAIHAHINKGSTPSMSTITHSAHMDIFONLAVDLDTBGRYLFPLNAI 2035
QY 133 ANOLRYPNSHHTYFSCCTMLYLFPAEANTEALIOEQITVLLERLIVNRPHPWGLITFIELI 192
|||||
DB 2036 ANOLRYPNSHHTYFSCCTMLYLFPAEANTEALIOEQITVLLERLIVNRPHPWGLITFIELI 2095
QY 193 KNPAKFMNHEFVHCAPBIEKLFQSVAOCCMGOKAQOVMEGTGAS 238
|||||
DB 2096 KNPAKFMNHEFVHCAPBIEKLFQSVAOCCMGOKAQOVMEGTGAS 2141

RESULT 5
US-10-690-276-10
; Sequence 10, Application US/10690276
; Publication No. US2005011218A1
; GENERAL INFORMATION:
; APPLICANT: Myriad Genetics, Incorporated
; APPLICANT: Climbora, Daniel
; APPLICANT: Heichman, Karen
; APPLICANT: Bartel, Paul
; APPLICANT: Mauck, Kimberly
; APPLICANT: Bush, Angie
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING INFLAMMATORY DISORDERS
; FILE REFERENCE: 1834.01
; CURRENT APPLICATION NUMBER: US/10/690,276
; CURRENT FILING DATE: 2003-10-20
; PRIOR APPLICATION NUMBER: 09/727,384
; PRIOR FILING DATE: 2000-12-01
; PRIOR APPLICATION NUMBER: 60/168,377
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: 60/168,379
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: 60/185,056
; PRIOR FILING DATE: 2000-02-25
; PRIOR APPLICATION NUMBER: 10/035,344
; PRIOR FILING DATE: 2002-01-04
; PRIOR APPLICATION NUMBER: 60/259,571
; PRIOR FILING DATE: 2001-01-04
; PRIOR APPLICATION NUMBER: 10/035,343
; PRIOR FILING DATE: 2002-01-04
; PRIOR APPLICATION NUMBER: 60/259,572
; PRIOR FILING DATE: 2001-01-04
; PRIOR APPLICATION NUMBER: 10/099,924
; PRIOR FILING DATE: 2002-03-14
; PRIOR APPLICATION NUMBER: 60/276,179
; PRIOR FILING DATE: 2001-03-15
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 728
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 10
; LENGTH: 2141
; TYPE: PR1
; ORGANISM: Homo sapiens
US-10-690-276-10

Query Match 94.8%; Score 1178; DB 17; Length 2141;
Best Local Similarity 99.6%; Pred. No. 3e-116;
Matches 225; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 13 QVDMLESEINIAPIRLTNFTGVMPPQFKDLSYLTXTSPVTFSLDLSNLOVSNBGNRY 72
:|||||
DB 1916 KVMLESEINIAPIRLTNFTGVMPPQFKDLSYLTXTSPVTFSLDLSNLOVSNBGNRY 1975
QY 73 NQOLINALVLYVGTQAIHAHINKGSTPSMSTITHSAHMDIFONLAVDLDTBGRYLFPLNAI 132
|||||
DB 1976 NQOLINALVLYVGTQAIHAHINKGSTPSMSTITHSAHMDIFONLAVDLDTBGRYLFPLNAI 2035
```

```
QY 133 ANOLRYPNSHHTYFSCCTMLYLFPAEANTEALIOEQITVLLERLIVNRPHPWGLITFIELI 192
|||||
DB 2036 ANOLRYPNSHHTYFSCCTMLYLFPAEANTEALIOEQITVLLERLIVNRPHPWGLITFIELI 2095
QY 193 KNPAKFMNHEFVHCAPBIEKLFQSVAOCCMGOKAQOVMEGTGAS 238
|||||
DB 2096 KNPAKFMNHEFVHCAPBIEKLFQSVAOCCMGOKAQOVMEGTGAS 2141

RESULT 6
US-10-144-194A-72
; Sequence 72, Application US/10144194A
; Publication No. US20030215809A1
; GENERAL INFORMATION:
; APPLICANT: Origene Technologies Inc
; TITLE OF INVENTION: Regulated Breast Cancer Genes
; FILE REFERENCE: 3U 103 R1
; CURRENT APPLICATION NUMBER: US/10/144,194A
; CURRENT FILING DATE: 2002-06-12
; NUMBER OF SEQ ID NOS: 114
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 72
; LENGTH: 2376
; TYPE: PR1
; ORGANISM: Homo sapiens
US-10-144-194A-72

Query Match 94.8%; Score 1178; DB 15; Length 2376;
Best Local Similarity 99.6%; Pred. No. 3.4e-116;
Matches 225; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 13 QVDMLESEINIAPIRLTNFTGVMPPQFKDLSYLTXTSPVTFSLDLSNLOVSNBGNRY 72
:|||||
DB 2151 KVMLESEINIAPIRLTNFTGVMPPQFKDLSYLTXTSPVTFSLDLSNLOVSNBGNRY 2210
QY 73 NQOLINALVLYVGTQAIHAHINKGSTPSMSTITHSAHMDIFONLAVDLDTBGRYLFPLNAI 132
|||||
DB 2211 NQOLINALVLYVGTQAIHAHINKGSTPSMSTITHSAHMDIFONLAVDLDTBGRYLFPLNAI 2270
QY 133 ANOLRYPNSHHTYFSCCTMLYLFPAEANTEALIOEQITVLLERLIVNRPHPWGLITFIELI 192
|||||
DB 2271 ANOLRYPNSHHTYFSCCTMLYLFPAEANTEALIOEQITVLLERLIVNRPHPWGLITFIELI 2330
QY 193 KNPAKFMNHEFVHCAPBIEKLFQSVAOCCMGOKAQOVMEGTGAS 238
|||||
DB 2331 KNPAKFMNHEFVHCAPBIEKLFQSVAOCCMGOKAQOVMEGTGAS 2376

RESULT 7
US-10-491-566-72
; Sequence 72, Application US/10491566
; Publication No. US2004024914A1
; GENERAL INFORMATION:
; APPLICANT: Origene Technologies Inc
; TITLE OF INVENTION: Regulated Breast Cancer Genes
; FILE REFERENCE: 3U 103 R1
; CURRENT APPLICATION NUMBER: US/10/491,566
; CURRENT FILING DATE: 2004-04-05
; NUMBER OF SEQ ID NOS: 148
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 72
; LENGTH: 2376
; TYPE: PR1
; ORGANISM: Homo sapiens
US-10-491-566-72

Query Match 94.8%; Score 1178; DB 16; Length 2376;
Best Local Similarity 99.6%; Pred. No. 3.4e-116;
Matches 225; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 13 QVDMLESEINIAPIRLTNFTGVMPPQFKDLSYLTXTSPVTFSLDLSNLOVSNBGNRY 72
:|||||
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Db 2151 KYDMLSEINIAPRLITNFTGVMPPOPKDLSYIKTRSPVTFSLDLSRNLQVSNBGNRY 2210  
QY 73 NQOLINALVYVGTQALIAHINKGSTPSMSTITHSAHMDIFQNLAVDLDTBGRYLFNAI 132  
Db 2211 NQOLINALVYVGTQALIAHINKGSTPSMSTITHSAHMDIFQNLAVDLDTBGRYLFNAI 2270  
QY 133 ANQLRYPNSHTYFSCITMLYLPFAEANTEALIOEQITRVLLERLIYNRPHPWGLITFIELI 192  
Db 2271 ANQLRYPNSHTYFSCITMLYLPFAEANTEALIOEQITRVLLERLIYNRPHPWGLITFIELI 2330  
QY 193 KNPAPKFNHNEFVHCAPRIEKLFGSVAAQCCMGQKQAQVMEGTGA 238  
Db 2331 KNPAPKFNHNEFVHCAPRIEKLFGSVAAQCCMGQKQAQVMEGTGA 2376

## RESULT 8

US-10-369-493-5760  
Sequence 5760, Application US/10369493  
Publication No. US20030233675A1  
GENERAL INFORMATION:  
APPLICANT: Cao, Yongwei  
APPLICANT: Hinkle, Gregory J.  
APPLICANT: Slater, Steven C.  
APPLICANT: Goldman, Barry S.  
APPLICANT: Chen, Xianfeng  
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF  
FILE REFERENCE: 38-10(52052)B  
CURRENT APPLICATION NUMBER: US/10/369,493  
CURRENT FILING DATE: 2003-02-28  
PRIOR APPLICATION NUMBER: US 60/360,039  
PRIOR FILING DATE: 2002-02-21  
NUMBER OF SEQ ID NOS: 47374  
SEQ ID NO 5760  
LENGTH: 2500  
TYPE: PRT  
ORGANISM: Caenorhabditis elegans  
US-10-369-493-5760

## Query Match

Beet Local Similarity 52.5%; Score 653; DB 15; Length 2500;  
Matches 121; Conservative 34; Mismatches 70; Indels 0; Gaps 0;

QY 13 QVDMLSEINIAPRLITNFTGVMPPOPKDLSYIKTRSPVTFSLDLSRNLQVSNBGNRY 72  
Db 2256 QVDITPEMAVEBKSNLNMATIIIPDIRILDEYLANRISVDPILPILQONQAGTKY 2315  
QY 73 NQOLINALVYVGTQALIAHINKGSTPSMSTITHSAHMDIFQNLAVDLDTBGRYLFNAI 132  
Db 2316 NQOLINALVYVGTQALIAHINKGSTPSMSTITHSAHMDIFQNLAVDLDTBGRYLFNAI 2375  
QY 133 ANQLRYPNSHTYFSCITMLYLPFAEANTEALIOEQITRVLLERLIYNRPHPWGLITFIELI 192  
Db 2376 ANQLRYPNSHTYFSCITMLYLPFAEANTEALIOEQITRVLLERLIYNRPHPWGLITFIELI 2435  
QY 193 KNPAPKFNHNEFVHCAPRIEKLFGSVAAQCCMGQKQAQVMEGTGA 237  
Db 2436 KNPAPKFNHNEFVHCAPRIEKLFGSVAAQCCMGQKQAQVMEGTGA 2480

## RESULT 9

US-10-424-599-180820  
Sequence 180820, Application US/10424599  
Publication No. US20040031072A1  
GENERAL INFORMATION:  
APPLICANT: La Rosa Thomas J  
APPLICANT: Kovalic David K  
APPLICANT: Zhou Yihua  
APPLICANT: Cao Yongwei  
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated with  
FILE REFERENCE: 38-21(53223)B  
CURRENT APPLICATION NUMBER: US/10/424,599

; CURRENT FILING DATE: 2003-04-28  
; NUMBER OF SEQ ID NOS: 285684  
; SEQ ID NO 180820  
; LENGTH: 394  
; TYPE: PRT  
; ORGANISM: glycine max  
; FEATURE:  
; OTHER INFORMATION: Clone ID: PAT\_MRT3847\_134295C.1.pcp  
US-10-424-599-180820

Query Match 52.2%; Score 648.5; DB 15; Length 394;  
Beet Local Similarity 60.1%; Pred. No. 1.7e-60;  
Matches 140; Conservative 23; Mismatches 49; Indels 21; Gaps 7;

QY 17 LSEINIAPRLITNFTGVMPPOPKDLSYIKTRSPVTFSLDLSRNLQVSNBGNRY 68  
Db 161 LRETTQSPRLISEVDAAKAKOMKVDVEYIKTRQOSP--FLSELKOKLISPEEASA 218  
QY 69 GNRVNLQINALVYVGTQALIAHINKGSTPSMSTITHSAHMDIFQNLAVD 119  
Db 219 GNRVNLQINALVYVGTQALIAHINKGSTPSMSTITHSAHMDIFQNLAVD 276  
QY 120 LDTBGRYLFNAIANQLRYPNSHTYFSCITMLYLPFAEANTEALIOEQITRVLLERLIYNRP 179  
Db 277 LDTBGRYLFNAIANQLRYPNSHTYFSCITMLYLPFAEANTEALIOEQITRVLLERLIYNRP 336  
QY 180 HPWGLITFIELIKNPAPKFNHNEFVHCAPRIEKLFGSVAAQCCMGQKQAQVMEGTGA 232  
Db 337 HPWGLITFIELIKNPAPKFNHNEFVHCAPRIEKLFGSVAAQCCMGQKQAQVMEGTGA 389

## RESULT 10

US-10-425-114-59023  
Sequence 59023, Application US/10425114  
Publication No. US20040034888A1  
GENERAL INFORMATION:  
APPLICANT: Liu, Jindong  
APPLICANT: Zhou, Yihua  
APPLICANT: Kovalic, David K.  
APPLICANT: Screen, Steven E.  
APPLICANT: Tabaska, Jack E.  
APPLICANT: Cao, Yongwei  
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with  
FILE REFERENCE: 38-21(53313)B  
CURRENT APPLICATION NUMBER: US/10/425,114  
CURRENT FILING DATE: 2003-04-28  
NUMBER OF SEQ ID NOS: 73128  
SEQ ID NO 59023  
LENGTH: 683  
TYPE: PRT  
ORGANISM: Zea mays  
FEATURE:  
OTHER INFORMATION: Clone ID: 700096523\_FLI.pcp  
US-10-425-114-59023

Query Match 51.6%; Score 641; DB 15; Length 683;  
Beet Local Similarity 57.1%; Pred. No. 2.3e-59;  
Matches 136; Conservative 27; Mismatches 55; Indels 20; Gaps 6;

QY 13 QVDMLSEINIAPRLITNFTGVMPPOPKDLSYIKTRSPVTFSLDLSRNLQVSNBGNRY 67  
Db 442 KIDDLAELISINAPRIMSVDGALKSKQKTEVDEYIKRPEGSSFLSDNQLKLLQONBASV 501  
QY 68 PGNRYNLQINALVYVGTQALIAHINKGSTPSMSTITHSAHMDIFQNLAVD 116  
Db 502 AGTRVNLQINALVYVGTQALIAHINKGSTPSMSTITHSAHMDIFQNLAVD 561  
QY 117 AVDLDTBGRYLFNAIANQLRYPNSHTYFSCITMLYLPFAEANTEALIOEQITRVLLERLIYNRP 176  
Db 562 ITSDTBGRYLFNAIANQLRYPNSHTYFSCITMLYLPFAEANTEALIOEQITRVLLERLIYNRP 621  
QY 177 NRHPWGLITFIELIKNPAPKFNHNEFVHCAPRIEKLFGSVAAQCCMGQKQAQVMEGTGA 234



```
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 192119
; LENGTH: 443
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(443)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_106798C.1.pep
US-10-425-115-192119
```

Query Match 49.7%; Score 617.5; DB 16; Length 443;  
Best Local Similarity 56.9%; Pred. No. 4.2e-57;  
Matches 136; Conservative 28; Mismatches 54; Indels 21; Gaps 8;

```
QY 13 QVDMSEINIAPIRLNFTGVM-PPQFKDLSYLTGRSPVTFPLSDLRSLQV-SNE--- 67
   ::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
DB 201 KIDLAEISIAPIRIMSDVDGTLSKQKTEBDEYLTGRPGSSFLVKQNLPLPQNEAAV 260
   |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
QY 68 PGNRYNLQILNALVLYVGTQAIHAI-HNK-GSTPSMSTITHSAHMDIFQ-----NL 116
   |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
DB 261 AGTRYVNPILNSLVLYGIAVQQLQONKANASASVQIKHPTMDSFQIETATEMPTNL 320
   |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
QY 117 AVDLPTGKRYLFLNAINQRLRYNSHTYFSCMTLYLPAA-NTEAIOEQITRVLLERLI 175
   |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
DB 321 ITSPDTGKRYLFLNAINQRLRYNSHTYFPIIHLFPAATQXKIIQEQITRVLLERLI 380
   |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
QY 176 VNRPHPMGLITFIELIKNPAPKFWNHEFVHCAPETIKLFQSVAOCCMGQKQAOQVMEG 234
   |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
DB 381 VNRPHPMGLITFIELIKNPRIYFNWRSFTHSAPETIKLFESVARS-C---GAKAVDEG 435
   |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
```

```
RESULT 15
US-10-425-114-37764
; Sequence 37764, Application US/10425114
; Publication No. US20040034868A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jindong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaka, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 37764
; LENGTH: 443
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB3245-490-C9_FLI.pep
US-10-425-114-37764
```

Query Match 49.6%; Score 616.5; DB 15; Length 443;  
Best Local Similarity 56.9%; Pred. No. 5.4e-57;  
Matches 136; Conservative 28; Mismatches 54; Indels 21; Gaps 8;

```
QY 13 QVDMSEINIAPIRLNFTGVM-PPQFKDLSYLTGRSPVTFPLSDLRSLQV-SNE--- 67
   ::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
```

```
DB 201 KIDLAEISIAPIRIMSDVDGTLSKQKTEBDEYLTGRPGSSFLVKQNLPLPQNEAAV 260
QY 68 PGNRYNLQILNALVLYVGTQAIHAI-HNK-GSTPSMSTITHSAHMDIFQ-----NL 116
   |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
DB 261 AGTRYVNPILNSLVLYGIAVQQLQONKANASASVQIKHPTMDSFQIETATEMPTNL 320
   |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
QY 117 AVDLPTGKRYLFLNAINQRLRYNSHTYFSCMTLYLPAA-NTEAIOEQITRVLLERLI 175
   |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
DB 321 ITSPDTGKRYLFLNAINQRLRYNSHTYFPIIHLFPAATQXKIIQEQITRVLLERLI 380
   |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
QY 176 VNRPHPMGLITFIELIKNPAPKFWNHEFVHCAPETIKLFQSVAOCCMGQKQAOQVMEG 234
   |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
DB 381 VNRPHPMGLITFIELIKNPRIYFNWRSFTHSAPETIKLFESVARS-C---GAKAVDEG 435
   |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
```

Search completed: July 14, 2005, 20:37:44  
Job time : 74.2171 secs



GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: July 14, 2005, 20:14:28 ; Search time 16.3411 Seconds

(without alignments)  
1401.351 Million cell updates/sec

Title: US-10-019-151C-1

Perfect score: 1243

Sequence: 1 MILLVILAFYLMQVDMSEI.....AGCCMGQKQAOVMEGTGAS 238

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: PIR.79:\*  
2: PIR1:\*  
3: PIR2:\*  
4: PIR3:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1178	94.8	1100	T17270	hypothetical prote
2	653	52.5	2500	G88493	protein F57B9.2 [1
3	615.5	49.5	1865	G86152	T1723.15 protein -
4	317	25.5	2100	T38128	CT123.15 protein -
5	231.5	18.6	2108	S28417	CDK39 protein - ye
6	95.5	7.7	2819	A90551	conserved hypochet
7	90	7.2	240	B64461	hypothetical prote
8	86	6.9	251	F89929	hypothetical prote
9	86	6.9	414	G89862	NAD-specific gluta
10	84.5	6.8	1125	S67794	probable membrane
11	83.5	6.7	378	E59094	hypothetical prote
12	83.5	6.7	378	T25176	hypothetical prote
13	83	6.7	350	AH3020	conserved hypochet
14	83	6.7	350	A98264	hypothetical 33.7K
15	82.5	6.6	428	H96641	hypothetical prote
16	82.5	6.6	536	S15183	gas-vesicle operon
17	82.5	6.6	536	T08241	gas-vesicle operon
18	82.5	6.6	781	T18693	hypothetical prote
19	81.5	6.6	733	T03117	glycoprotein H - a
20	81.5	6.6	536	G88954	protein K04P1.13 [
21	81.5	6.6	1039	B71342	hypothetical prote
22	81	6.5	263	T16329	hypothetical prote
23	81	6.5	312	F64435	mevalonate kinase
24	80.5	6.5	411	AD1342	ABC transporter (m
25	80	6.4	367	T13649	lipoprotein - Acti
26	80	6.4	658	H90013	hypothetical prote
27	79.5	6.4	336	T26993	hypothetical prote
28	79.5	6.4	552	J01788	DNA ligase (ATP) (
29	79.5	6.4	552	WNV27W	DNA ligase (ATP) (

30	79.5	6.4	1034	2	A82563	acetylflavin resista
31	79.5	6.4	1799	2	AD1895	serine/threonine k
32	79.5	6.4	2332	1	GNNTR	genome polypotein
33	79	6.4	354	2	C89860	hypothetical prote
34	79	6.4	492	2	C84142	hypothetical prote
35	79	6.4	560	2	S29307	poly(3-hydroxyalka
36	79	6.4	638	2	B34285	NADH2 dehydrogenas
37	79	6.4	830	2	S55940	factor arrest prot
38	79	6.4	1015	2	B84458	probable retroelem
39	78.5	6.3	376	2	A44940	actin - pork tapew
40	78.5	6.3	890	1	J01947	genome polypotein
41	78	6.3	462	2	S10439	DNA-directed RNA p
42	78	6.3	529	2	B84813	hypothetical prote
43	78	6.3	558	1	MMXRT	RNA 10 protein - r
44	78	6.3	575	2	S72283	DNA-directed RNA p
45	78	6.3	700	2	B69146	sensory transducti

#### ALIGNMENTS

##### RESULT 1

T17270 hypothetical protein DKFP434N241.1 - human (fragment)

C:Species: Homo sapiens (man)

C>Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 09-Jul-2004

C/Accession: T17270

R/Poussack, A.; Klein, M.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.

submitted to the Protein Sequence Database, September 1999

A/Reference number: Z18723

A/Accession: T17270

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-1100 <POU>

A/Cross-references: UNIPROT:Q9UPR8; EMBL:AL117492

A/Experimental source: adult testis; clone DKFP434N241

A/Genetics:

A/Note: DKFP434N241.1

Query Match 94.8%; Score 1178; DB 2; Length 1100;  
Best local similarity 99.6%; Pred. No. 5.1e-97;  
Matches 225; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY	13	QVDMSEINAPILINFTGVMPPOKQDLSLTKRSPVTPISDLSNLOVSENGRNY 72
DB	875	KVDMSEINAPILINFTGVMPPOKQDLSLTKRSPVTPISDLSNLOVSENGRNY 934
QY	73	NLOINAVLYVGTQAIHAIHNKSTPMSSTTHSAMDFONLAVDLOTEGRYLPINAI 132
DB	935	NLOINAVLYVGTQAIHAIHNKSTPMSSTTHSAMDFONLAVDLOTEGRYLPINAI 994
QY	133	ANOLRYPNSTHFTSCMLYLPFAANTEAIQEOITVLERLIVNRPWGLITPTELI 192
DB	995	ANOLRYPNSTHFTSCMLYLPFAANTEAIQEOITVLERLIVNRPWGLITPTELI 1054
QY	193	KNDAPFVWNEFVHCAPBIEIKLFQSYAQCCKGQKQAOVMEGTGAS 238
DB	1055	KNDAPFVWNEFVHCAPBIEIKLFQSYAQCCKGQKQAOVMEGTGAS 1100

##### RESULT 2

G88493 protein F57B9.2 (imported) - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C>Date: 10-May-2001 #sequence\_revision 10-May-2001 #text\_change 09-Jul-2004

C/Accession: G88493

R/anonymous, The C. elegans Sequencing Consortium.

Science 282, 2012-2018, 1998

A/Title: Genome sequence of the nematode C. elegans: a platform for investigating biolo

A/Reference number: A75000; WUID:99069613; PMID:9851916

A/Note: see websites genome.wustl.edu/gsc/C.elegans/ and www.sanger.ac.uk/Projects/C\_el

A/Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; am

A/Accession: G88493



```

A:Reference number: S19415
A:Accession: S19770
A:Molecule type: DNA
A:Residues: 1852-2107 <LIN>
A:Cross-references: EMBL:X59720, MIPS:YCR093w
C:Genetics:
A:Gene: SGD:CDG3
A:Cross-references: SGD:S0000689, MIPS:YCR093w
A:Map position: 3R
C:Keywords: nucleus; transcription regulation; transmembrane protein
P:122-38/Domain: transmembrane #status predicted <TM1>
P:1269-286/Domain: transmembrane #status predicted <TM2>
P:1342-335/Domain: transmembrane #status predicted <TM3>
P:1386-402/Domain: transmembrane #status predicted <TM4>
P:1562-578/Domain: transmembrane #status predicted <TM5>
P:1663-680/Domain: transmembrane #status predicted <TM6>
P:1783-801/Domain: transmembrane #status predicted <TM7>
P:1843-855/Domain: transmembrane #status predicted <TM8>
P:1849-1455/Domain: transmembrane #status predicted <TM9>
P:1835-1656/Domain: transmembrane #status predicted <TM10>
P:1865-1681/Domain: transmembrane #status predicted <TM11>
P:1751-1767/Domain: transmembrane #status predicted <TM12>
P:1773-1789/Domain: transmembrane #status predicted <TM13>
P:1801-1817/Domain: transmembrane #status predicted <TM14>
P:1928-1944/Domain: transmembrane #status predicted <TM15>

Query Match      18.6%; Score 231.5; DB 2; Length 2108;
Best Local Similarity 32.6%; Pred. No. 5; 4e-12;
Matches 63; Conservative 40; Mismatches 77; Indels 13; Gaps 6;

Cy 39 KKLDLSYLKTRSPV---TFSLDL--RSNIQVSNEPRNRK---NLGLINLVTVYGTQAIAH 91
Db 1890 KKPVDNVIYRIISNSLLRTILTAIXKYDYDIKKGVGYPLSVDSKLIRAIIVAHGIE--AG 1947

Cy 92 IHNKGSTPSMSTITHSAMDIFONLAVDLTREGRLFLNAIAYALDRYPNSHTHFESCTML 151
Db 1948 IEKRTSSNAVPTKKSITYTLFNLIONGSIEMKQQIILSIVEQLRPNIHTPFSEVLAM 2007

Cy 152 YLFPA--EANTB-AIOBITREULLERLIYNRPHPGGLITPEIBLIKDPAPKFNHHEFYHC 207
Db 2008 NMFPSDENNDCKLENGOELLINPLKRILIVNKPHTWGVSVPFTQILINNDDIMLDLPFGQS 2067

Cy 208 APEIEKLFQSVAAQ 220
Db 2068 VPEIKTILQCLVK 2080

RESULT 6
A:90551
conserved hypothetical protein MYPU_3130 [imported] - Mycoplasma pulmonis (strain UAB CT)
C:Species: Mycoplasma pulmonis
C:Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 09-Jul-2004
C:Accession: A90551
P:Chambud, J., Hellig, R.; Ferris, S.; Barbe, V.; Samson, D.; Galissou, F.; Moszer, I. N.
Nucleic Acids Res. 29, 2145-2153, 2001
A>Title: The complete genome sequence of the murine respiratory pathogen Mycoplasma pulmonis
A:Reference number: A95512; MUID:21267165; PMID:11353084
A:Accession: A90551
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-2819 <KUR>
A:Cross-references: UNIPROT:Q980P8, GB:AL445566; PID:g14089727; PIND:CAIC13486.1; GSPDB:G
A:Experimental source: strain UAB CTIP
C:Genetics:
A:Gene: MYPU_3130
A:Genetic code: SGCC3

Query Match      7.7%; Score 95.5; DB 2; Length 2819;
Best Local Similarity 25.2%; Pred. No. 12;
Matches 62; Conservative 33; Mismatches 86; Indels 65; Gaps 12;

Cy 14 VDMUSEINIADRIILTNTFTGWMP---PPPK-KDLDLSYLK--TRSPVFSLD-----L 58

```

Db 2056 IDALSTNIVAEKLEVFLEAVKXKQNPQSKTNDLFASIGELIKSKSPDPSQNGPLFVLTSTIL 2115

Qy 59 RSNLOVSNPEGRNYNLQILNALV-----LYVGTQIAHI-----HNK----- 95

Db 2116 KSNILDSKSIINKEKIKVKTLPFEKLKMTSVQNFVKDPTENISKSIPIDONNQSLSK 2175

Qy 96 -----GSTPSNSTITTHSAHMDIPQN-----LAVDLDEGRVLT--FLNAINQ 135

Db 2176 IVALIADDPQTTNLVNVKVIDIDIFQNHKNYASKANLNLITAEPLTTHKNQLAVALKSTILNK 2235

Qy 136 LRYNSHTHYESSCTML--YLFAEANTB---AIOEQTITVLE--RLIVNRPHPMGLITTF 188

Db 2236 LNVVSESLHDPSSVNVVLSQLSKSNIEFNNEKESQLSILKTSIHLINSDIPOLVANNL 2295

Qy 189 IELIKN 194

Db 2296 IEEIKN 2301

RESULT 7

B64461

hypothetical protein MJ1291 - Methanococcus jannaschii

C:Species: Methanococcus jannaschii

C:Date: 13-Sep-1996 #sequence\_revision 13-Sep-1996 #text\_change 04-Mar-2000

C:Accession: B64461

R:Butt, C.J.; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, G.G.; Blake, R.; Reich, C.I.; Overbeek, R.; Kirkness, E.F.; Weissbrock, K.G.; Merrick, J.M.; Glodek, A.; Tsion, J.D.; Sedow, P.W.; Hanna, M.C.; Cotton, M.D.; Roberts, K.M.; Hurel, M.A. Science 273, 1058-1073, 1996

A:Authors: Kaine, B.P.; Borodovsky, M.; Klenk, H.P.; Fraser, C.M.; Smith, H.O.; Moese, A. Title: Complete genome sequence of the methanogenic archaeon, Methanococcus jannaschii A:Reference number: A64300, MUID:96337999; PMID:868087

A:Accession: B64461

A:Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-240 <BLU>

A:Cross-references: GB:U67569, GB:L77117, NID:g1591918, PID:g1591928, TIGR:MJ1291, PID: C:Genetic8:

C:Map position: REV1238450-1237728

C:Superfamily: Methanococcus jannaschii hypothetical protein MJ1291

Query Match 7.2%; Score 90; DB 2; Length 240;

Best Local Similarly 1.7%; Pred. No. 1.4;

Matches 47; Conservative 37; Mismatches 83; Indels 50; Gaps 9;

Qy 3 LVLVIATYLMQVMDLSRI--NIAPRILTNFGVMPQPKKOLDGYLKTSPVTFSLDLS 60

Db 20 IVGAATYAAVSNKVPFSPTTEKTIPTTKSSIGNIKKPIEISTLETYYFTN-----LDLNG 73

Qy 61 NLGVSNPEGRNYNLQILNALVLYGVTOAIIHNKGS-----TPSMSTITTHSAH 109

Db 74 DSNITNNPER-----PIQTIKAFINNIDSDLNKNTIRIYCYCTPVSNAASVAVID 122

Qy 110 MDIFQNLAVLDLT---EGRYLFLNAINQRLKRPNSHTHYESSCTMLYFLPEANTEAIOE 164

Db 123 -DSSNNMLLDREDEPNYVSGQYVYFNGTV---YSSMKFEDENGKLFYAAASGNALN- 176

Qy 165 QITRVLLERLIVNRPHWGL-----ITFELIKN 194

Db 177 --TSNMLDLIDLNCPTESFLKNGSKTDIYVILINN 211

RESULT 8

P89929

hypothetical protein BA1333 [imported] - Staphylococcus aureus (strain N315)

C:Species: Staphylococcus aureus

C:Date: 10-May-2001 #sequence\_revision 10-May-2001 #text\_change 09-Jul-2004

C:Accession: P89929

R:Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Gui, L.; Oguni, A.; Mizutani-Uji, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.; Shiba, T.; Hattori, K.; Ogasawara, S.; Hayashi, H.; Hirataezu, K. J. Bacteriol 187, 1225-1240, 2001

Query Match 7.2%; Score 90; DB 2; Length 240;

Best Local Similarly 1.7%; Pred. No. 1.4;

Matches 47; Conservative 37; Mismatches 83; Indels 50; Gaps 9;

Qy 3 LVLVIATYLMQVMDLSRI--NIAPRILTNFGVMPQPKKOLDGYLKTSPVTFSLDLS 60

Db 20 IVGAATYAAVSNKVPFSPTTEKTIPTTKSSIGNIKKPIEISTLETYYFTN-----LDLNG 73

Qy 61 NLGVSNPEGRNYNLQILNALVLYGVTOAIIHNKGS-----TPSMSTITTHSAH 109

Db 74 DSNITNNPER-----PIQTIKAFINNIDSDLNKNTIRIYCYCTPVSNAASVAVID 122

Qy 110 MDIFQNLAVLDLT---EGRYLFLNAINQRLKRPNSHTHYESSCTMLYFLPEANTEAIOE 164

Db 123 -DSSNNMLLDREDEPNYVSGQYVYFNGTV---YSSMKFEDENGKLFYAAASGNALN- 176

Qy 165 QITRVLLERLIVNRPHWGL-----ITFELIKN 194

Db 177 --TSNMLDLIDLNCPTESFLKNGSKTDIYVILINN 211

Query Match 7.2%; Score 90; DB 2; Length 240;

Best Local Similarly 1.7%; Pred. No. 1.4;

Matches 47; Conservative 37; Mismatches 83; Indels 50; Gaps 9;

Qy 3 LVLVIATYLMQVMDLSRI--NIAPRILTNFGVMPQPKKOLDGYLKTSPVTFSLDLS 60

Db 20 IVGAATYAAVSNKVPFSPTTEKTIPTTKSSIGNIKKPIEISTLETYYFTN-----LDLNG 73

Qy 61 NLGVSNPEGRNYNLQILNALVLYGVTOAIIHNKGS-----TPSMSTITTHSAH 109

Db 74 DSNITNNPER-----PIQTIKAFINNIDSDLNKNTIRIYCYCTPVSNAASVAVID 122

Qy 110 MDIFQNLAVLDLT---EGRYLFLNAINQRLKRPNSHTHYESSCTMLYFLPEANTEAIOE 164

Db 123 -DSSNNMLLDREDEPNYVSGQYVYFNGTV---YSSMKFEDENGKLFYAAASGNALN- 176

Qy 165 QITRVLLERLIVNRPHWGL-----ITFELIKN 194

Db 177 --TSNMLDLIDLNCPTESFLKNGSKTDIYVILINN 211

Query Match 7.2%; Score 90; DB 2; Length 240;

Best Local Similarly 1.7%; Pred. No. 1.4;

Matches 47; Conservative 37; Mismatches 83; Indels 50; Gaps 9;

Qy 3 LVLVIATYLMQVMDLSRI--NIAPRILTNFGVMPQPKKOLDGYLKTSPVTFSLDLS 60

Db 20 IVGAATYAAVSNKVPFSPTTEKTIPTTKSSIGNIKKPIEISTLETYYFTN-----LDLNG 73

Qy 61 NLGVSNPEGRNYNLQILNALVLYGVTOAIIHNKGS-----TPSMSTITTHSAH 109

Db 74 DSNITNNPER-----PIQTIKAFINNIDSDLNKNTIRIYCYCTPVSNAASVAVID 122

Qy 110 MDIFQNLAVLDLT---EGRYLFLNAINQRLKRPNSHTHYESSCTMLYFLPEANTEAIOE 164

Db 123 -DSSNNMLLDREDEPNYVSGQYVYFNGTV---YSSMKFEDENGKLFYAAASGNALN- 176

Qy 165 QITRVLLERLIVNRPHWGL-----ITFELIKN 194

Db 177 --TSNMLDLIDLNCPTESFLKNGSKTDIYVILINN 211

Query Match 7.2%; Score 90; DB 2; Length 240;

Best Local Similarly 1.7%; Pred. No. 1.4;

Matches 47; Conservative 37; Mismatches 83; Indels 50; Gaps 9;

Qy 3 LVLVIATYLMQVMDLSRI--NIAPRILTNFGVMPQPKKOLDGYLKTSPVTFSLDLS 60

Db 20 IVGAATYAAVSNKVPFSPTTEKTIPTTKSSIGNIKKPIEISTLETYYFTN-----LDLNG 73

Qy 61 NLGVSNPEGRNYNLQILNALVLYGVTOAIIHNKGS-----TPSMSTITTHSAH 109

Db 74 DSNITNNPER-----PIQTIKAFINNIDSDLNKNTIRIYCYCTPVSNAASVAVID 122

Qy 110 MDIFQNLAVLDLT---EGRYLFLNAINQRLKRPNSHTHYESSCTMLYFLPEANTEAIOE 164

Db 123 -DSSNNMLLDREDEPNYVSGQYVYFNGTV---YSSMKFEDENGKLFYAAASGNALN- 176

Qy 165 QITRVLLERLIVNRPHWGL-----ITFELIKN 194

Db 177 --TSNMLDLIDLNCPTESFLKNGSKTDIYVILINN 211

Query Match 7.2%; Score 90; DB 2; Length 240;

Best Local Similarly 1.7%; Pred. No. 1.4;

Matches 47; Conservative 37; Mismatches 83; Indels 50; Gaps 9;

Qy 3 LVLVIATYLMQVMDLSRI--NIAPRILTNFGVMPQPKKOLDGYLKTSPVTFSLDLS 60

Db 20 IVGAATYAAVSNKVPFSPTTEKTIPTTKSSIGNIKKPIEISTLETYYFTN-----LDLNG 73

Qy 61 NLGVSNPEGRNYNLQILNALVLYGVTOAIIHNKGS-----TPSMSTITTHSAH 109

Db 74 DSNITNNPER-----PIQTIKAFINNIDSDLNKNTIRIYCYCTPVSNAASVAVID 122

Qy 110 MDIFQNLAVLDLT---EGRYLFLNAINQRLKRPNSHTHYESSCTMLYFLPEANTEAIOE 164

Db 123 -DSSNNMLLDREDEPNYVSGQYVYFNGTV---YSSMKFEDENGKLFYAAASGNALN- 176

Qy 165 QITRVLLERLIVNRPHWGL-----ITFELIKN 194

Db 177 --TSNMLDLIDLNCPTESFLKNGSKTDIYVILINN 211

Query Match 7.2%; Score 90; DB 2; Length 240;

Best Local Similarly 1.7%; Pred. No. 1.4;

Matches 47; Conservative 37; Mismatches 83; Indels 50; Gaps 9;

Qy 3 LVLVIATYLMQVMDLSRI--NIAPRILTNFGVMPQPKKOLDGYLKTSPVTFSLDLS 60

Db 20 IVGAATYAAVSNKVPFSPTTEKTIPTTKSSIGNIKKPIEISTLETYYFTN-----LDLNG 73

Qy 61 NLGVSNPEGRNYNLQILNALVLYGVTOAIIHNKGS-----TPSMSTITTHSAH 109

Db 74 DSNITNNPER-----PIQTIKAFINNIDSDLNKNTIRIYCYCTPVSNAASVAVID 122

Qy 110 MDIFQNLAVLDLT---EGRYLFLNAINQRLKRPNSHTHYESSCTMLYFLPEANTEAIOE 164

Db 123 -DSSNNMLLDREDEPNYVSGQYVYFNGTV---YSSMKFEDENGKLFYAAASGNALN- 176

Qy 165 QITRVLLERLIVNRPHWGL-----ITFELIKN 194

Db 177 --TSNMLDLIDLNCPTESFLKNGSKTDIYVILINN 211

Query Match 7.2%; Score 90; DB 2; Length 240;

Best Local Similarly 1.7%; Pred. No. 1.4;

Matches 47; Conservative 37; Mismatches 83; Indels 50





Best Local Similarity 21.9%; Pred. No. 9.6;  
Matches 51; Conservative 36; Mismatches 72; Indels 74; Gaps 12;

```

QY 26 ILTNPTGV--MPPQPKDLD---SYLKTSNP-----VTFILSDLRSLQVSNPGRNRYNLQ 75
DB 20 ILVLFAGIKIVPQGHRYVERPGRYRTLEPGNLIIPEPESIGSKGNVMEQ-----71
QY 76 LINALVLYGTQAIHAIHNKSGTSPMSITHSAMDIFQNLAVDLDTBGRYLEFLNALIANQ 135
DB 72 ----VHLIPTQEV-----ITR-----DNASVSADAVTFYQVLNAAQAA 105
QY 136 LRYNSHTHYFSCYMLYLPAA-----ANTEAIOEQITRVLRLIYNRPHPGLL 185
DB 106 YQISNQLQMAIENLTMTNINSVWGSMDELDSNRDAINDRLAVNDEAV-----GPMGIK 160
QY 186 ITFIELIKNPAPFKFNNHEFHCAPEIEKLFQSVAGCCMGOKAQ-QVMEGTGA 237
DB 161 VTRIE-IKD-----IAP-KDVLDSMAROMKAKEREKRAQVLEAEGA 199

```

## RESULT 15

H96641  
hypothetical protein T25B24.1 [imported] - Arabidopsis thaliana  
C:Species: Arabidopsis thaliana (mouse-ear cress)  
C:Date: 02-Mar-2001 #sequence\_revision 02-Mar-2001 #text\_change 09-Jul-2004  
C:Accession: H96641  
R:Rheologis, A.; Ecker, J.R.; Palm, C.J.; Pederspiel, N.A.; Kaul, S.; White, O.; Alonso,  
Chin, C.W.; Chung, M.K.; Com, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;  
ansen, N.F.; Hughes, B.; Hultzer, L.  
Nature 408, 816-820, 2000  
A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.  
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luo, J.S.; Maltf, R.; Marziani,  
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.  
A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,  
Ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.  
A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.  
A:Reference number: A86141; MUID:21016719; PMID:11130712  
A:Accession: H96641  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-428 <STO>  
A:Cross-references: UNIPROT:Q9SY86; GB:AB051173; NID:94585871; PIDN:AAD25544.1; GSPDB:GN  
C:Genetics:  
A:Gene: T25B24.1  
A:Map position: 1

Query Match 6.6%; Score 82.5; DB 2; Length 428;

Best Local Similarity 21.2%; Pred. No. 14;

Matches 48; Conservative 33; Mismatches 104; Indels 41; Gaps 9;

```

QY 9 FYIMQVDMLESEINARIILTNPTGVMPQPKDLDYIKTRSPVTFILSDLRSLQVSNP 68
DB 167 YMLSQVDLSREASHLSRFYINFRGMDVSPKPIYPLI--HPAVLVETYEHEGSVARYV 223
QY 69 GNRYNQLINALVLYGTQAIHAIHNKSGTSPMSITHSAMDIFQ-NLAVDLDTBGRYL 127
DB 224 DSGEGEKAKAKAHGTMALL-----KMLVDNFTHADMPGNILVRENNTRRGL 274
QY 128 FLNALINQLRYNSHTHYFSCYMLYLPAAANTE-----AIOEQITRVLRLI----- 175
DB 275 F-----RSRKHIVFLDVGMTAEISKTRDNLGPFKAVARRDGRTAABERTTLKLSKQ 326
QY 176 VNRPHPGLLITFIELIKNPAPFKFNNHE---PYHCAPEIEKLFQSV 218
DB 327 QNCPDPO---AFIKVEER-AFTFGTBEGLVHPADCMHELPEK 367

```

Search completed: July 14, 2005, 20:33:08  
Job time : 23.3411 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: July 14, 2005, 19:55:46 ; Search time 74.5891 Seconds

(without alignments)  
1633.949 Million cell updates/sec

Title: US-10-019-151C-1

Perfect score: 1243  
Sequence: 1 MILLVILAFYLMQVDMLESI.....AGCCMGKQKQAQVMEGTGAS 238

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : UniProt 03:\*  
1: uniprot\_sprot:\*  
2: uniprot\_trcemb:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1178	94.8	539	2	Q9BVZ6
2	1178	94.8	1100	2	Q9URR8
3	1178	94.8	1117	2	Q8K3D8
4	1178	94.8	1458	2	Q6ZQ08
5	1178	94.8	1620	2	Q8T853
6	1178	94.8	1835	2	Q9Y2I0
7	1178	94.8	2137	2	Q68DX7
8	1171	94.2	381	2	Q8C0H2
9	905.5	72.8	1872	2	Q7PW82
10	873	70.2	669	2	Q8IH39
11	873	70.2	2170	2	Q9V591
12	873	70.2	2172	2	Q8MKU3
13	794	63.9	424	2	Q8BX82
14	653	52.5	2500	2	Q20937
15	621.5	50.0	2363	2	Q94LQ9
16	615.5	49.5	682	2	Q84WS9
17	615.5	49.5	1865	2	Q81909
18	604.5	48.6	2526	2	Q75JL4
19	603	48.5	316	2	Q9U127
20	506.5	40.7	3371	2	Q81TW4
21	467.5	37.6	2589	2	Q7Y1I7
22	439	35.3	2145	2	Q67500
23	439	35.3	4466	2	Q81LS4
24	389.5	31.3	2017	2	Q6C0P0
25	381.5	30.7	463	2	Q7BM05
26	342	27.5	2223	2	Q6BQX3
27	323.5	26.0	947	2	Q7RK48
28	317	25.5	2100	2	P87112
29	270.5	21.8	1400	2	Q9N9L6
30	268.5	21.6	581	2	Q95TG6
31	256	20.6	2098	2	Q7S687

32	252	20.3	2141	2	Q75DB4	Q75DB4 aebhya gose
33	249	20.0	2140	2	Q6CSR0	Q6CSR0 kluyveromyc
34	231.5	18.6	2108	1	NOT1 YEAST	P25655 saccharomyc
35	215.5	17.3	2090	2	Q6TVN7	Q6TVN7 candida gla
36	107	8.6	1049	2	Q6TVY2	Q6TVY2 candida gla
37	97	7.8	524	2	Q6BVH7	Q6BVH7 debaryomyc
38	96	7.7	240	1	YC91 MERTJA	Q58687 methanococc
39	96	7.7	441	2	Q6CVU3	Q6CVU3 kluyveromyc
40	95.5	7.7	2819	2	Q98QP8	Q98QP8 mycoplasma
41	94.5	7.6	560	2	Q939A6	Q939A6 pseudomonas
42	94.5	7.6	1264	2	Q9ACB4	Q9ACB4 pseudomonas
43	94.5	7.6	473	1	Q7RPM6	Q7RPM6 plasmodium
44	93.5	7.5	473	1	SYC METTAC	Q818P6 methanocarc
45	92.5	7.4	355	2	Q8EHN8	Q8EHN8 shewanella

## ALIGNMENTS

RESULT 1  
Q9BVZ6 PRELIMINARY; PRT; 539 AA.  
ID Q9BVZ6  
AC Q9BVZ6;  
DT 01-JUN-2001 (TREMBlrel. 17, Created)  
DT 01-MAR-2004 (TREMBlrel. 26, Last sequence update)  
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)  
DE KIAA1007 protein (Fragment).  
GN Name=KIAA1007;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Placenta;  
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Straube R.L., Pelngold B.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buettow K.H., Schaefer C.F., Bhac N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hale F.,  
RA Diatchenko L., Marusha K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldi M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Usdin T.B., Tohyuki S., Carninci P., Prange C.,  
RA Baha S.S., Loggiano N.A., Peters G.J., Abramson R.D., Mulhally S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
RA Krzyzanski M.I., Skalska U., Smallus D.E., Schnerch A., Schein J.E.,  
RT Jones S.J., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
and mouse cDNA sequences.";  
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
[2]  
SEQUENCE FROM N.A.  
RC TISSUE=Placenta;  
RP Straube R.L.;  
RU Submitted (NCV-2000) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BC000779; AAH00779.2; -;  
DR InterPro; IPR001220; Lectin\_legB.  
DR Pfam; PF04054; Nccl1; 1.  
DR PROSITE; PS00307; LECTIN\_LEGUMB\_BETA; UNKNOWN\_1.  
FT NON\_TER 1 1  
SQ SEQUENCE 539 AA; 61829 MW; E59AB5187B1BDF5 CRC64;  
SO Query Match 94.8%; Score 1178; DB 2; Length 539;  
Best Local Similarity 99.6%; Pred. No. 3, 7e-94;  
Matches 225; Conservative 1; Mismatches 0; Indels 0; Gaps 0;



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QY 13 QVDMLESEINIAPIRLITNFTGVPMPQPKDLSYLTKTRSPVTLSDLRSMLOVSNBPNRY 72
DB 314 KIDMLSEINIAPIRLITNFTGVPMPQPKDLSYLTKTRSPVTLSDLRSMLOVSNBPNRY 373
QY 73 NIQLINALVLYVGTOAIAIHINKGSTPMSSTITHSAMDIQONLAVDLDTGGRYFLNMI 132
DB 374 NIQLINALVLYVGTOAIAIHINKGSTPMSSTITHSAMDIQONLAVDLDTGGRYFLNMI 433
QY 133 ANQLRPNSHHTYFSCMTLYLFAEANTEAIOEQITRVLLERLIIVNRPHPGLLITFIELI 192
DB 434 ANQLRPNSHHTYFSCMTLYLFAEANTEAIOEQITRVLLERLIIVNRPHPGLLITFIELI 493
QY 193 KNPAFFKFNHNEFVHCAPFEIKLFQSVAAQCCMGOKQAQVMEGTGAS 238
DB 494 KNPAFFKFNHNEFVHCAPFEIKLFQSVAAQCCMGOKQAQVMEGTGAS 539

RESULT 2
Q9UPR8 PRELIMINARY; PRT; 1100 AA.
ID Q9UPR8
AC Q9UPR8;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein DKFp434N241 (Fragment).
GN Name=DKFp434N241;
OS Homo sapiens (Human);
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxId=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Testis;
RA Pousetka A., Klein M., Mewes H.W., Gassenhuber J., Wiemann S.;
RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL117492; CAB55960.1; -.
DR PIR; T17270; T17270.
DR InterPro; IPR001220; Lectin_legb.
DR InterPro; IPR007196; Noct1.
DR Pfam; PF04054; Noct1; 1.
DR PROSITE; PS00307; LECTIN_LEGUME_BETA; UNKNOWN_1.
KW Hypothetical protein.
FT NON TER
SQ SEQUENCE 1100 AA; 124718 MW; 046DA23BD314A46F CRC64;

Query Match 94.8%; Score 1178; DB 2; Length 1100;
Best Local Similarity 99.6%; Pred. No. 8.8e-94;
Matches 225; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 13 QVDMLESEINIAPIRLITNFTGVPMPQPKDLSYLTKTRSPVTLSDLRSMLOVSNBPNRY 72
DB 875 KIDMLSEINIAPIRLITNFTGVPMPQPKDLSYLTKTRSPVTLSDLRSMLOVSNBPNRY 934
QY 73 NIQLINALVLYVGTOAIAIHINKGSTPMSSTITHSAMDIQONLAVDLDTGGRYFLNMI 132
DB 935 NIQLINALVLYVGTOAIAIHINKGSTPMSSTITHSAMDIQONLAVDLDTGGRYFLNMI 994
QY 133 ANQLRPNSHHTYFSCMTLYLFAEANTEAIOEQITRVLLERLIIVNRPHPGLLITFIELI 192
DB 995 ANQLRPNSHHTYFSCMTLYLFAEANTEAIOEQITRVLLERLIIVNRPHPGLLITFIELI 1054
QY 193 KNPAFFKFNHNEFVHCAPFEIKLFQSVAAQCCMGOKQAQVMEGTGAS 238
DB 1055 KNPAFFKFNHNEFVHCAPFEIKLFQSVAAQCCMGOKQAQVMEGTGAS 1100

RESULT 3
Q8K3D8 PRELIMINARY; PRT; 1117 AA.
ID Q8K3D8
AC Q8K3D8;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)

```

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DE RIKEN cDNA 6030411K04.
GN Name=6030411K04Rik;
OS Mus musculus (Mouse);
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Mammary tumor;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feilgold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Scheiner G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Schetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hultk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahney J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butlerfield Y.S.,
RA Krzywinski M.I., Skalka U., Smallos D.E., Scherch A., Schein J.E.,
RA Jones S.J., Matra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Mammary tumor;
RA Strausberg R.;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC018281; AAH18281.1; -.
DR MGD; MG1:2442402; 6030411K04Rik.
DR InterPro; IPR001220; Lectin_legb.
DR InterPro; IPR007196; Noct1.
DR Pfam; PF04054; Noct1; 1.
DR PROSITE; PS00307; LECTIN_LEGUME_BETA; UNKNOWN_1.
SQ SEQUENCE 1117 AA; 126687 MW; 49AD7FF80D49D97 CRC64;

Query Match 94.8%; Score 1178; DB 2; Length 1117;
Best Local Similarity 99.6%; Pred. No. 9e-94;
Matches 225; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 13 QVDMLESEINIAPIRLITNFTGVPMPQPKDLSYLTKTRSPVTLSDLRSMLOVSNBPNRY 72
DB 892 KIDMLSEINIAPIRLITNFTGVPMPQPKDLSYLTKTRSPVTLSDLRSMLOVSNBPNRY 951
QY 73 NIQLINALVLYVGTOAIAIHINKGSTPMSSTITHSAMDIQONLAVDLDTGGRYFLNMI 132
DB 952 NIQLINALVLYVGTOAIAIHINKGSTPMSSTITHSAMDIQONLAVDLDTGGRYFLNMI 1011
QY 133 ANQLRPNSHHTYFSCMTLYLFAEANTEAIOEQITRVLLERLIIVNRPHPGLLITFIELI 192
DB 1012 ANQLRPNSHHTYFSCMTLYLFAEANTEAIOEQITRVLLERLIIVNRPHPGLLITFIELI 1071
QY 193 KNPAFFKFNHNEFVHCAPFEIKLFQSVAAQCCMGOKQAQVMEGTGAS 238
DB 1072 KNPAFFKFNHNEFVHCAPFEIKLFQSVAAQCCMGOKQAQVMEGTGAS 1117

RESULT 4
Q6ZQ08 PRELIMINARY; PRT; 1458 AA.
ID Q6ZQ08
AC Q6ZQ08;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE KIAA1007 protein (Fragment).
GN Name=KIAA1007;

```



```

OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Embryonic tail;
RX PubMed=14621295;
RA Okazaki N., Kikuno R., Ohara R., Inamoto S., Koseki H., Hiraoka S.,
RA Suga Y., Nagase T., Ohara O., Koga H.;
RT "Prediction of the coding sequences of mouse homologues of KIA gene:
RT III. the complete nucleotide sequences of 500 mouse KIAA-homologous
RT cDNAs identified by screening of terminal sequences of cDNA clones
RT randomly sampled from size-fractionated libraries.";
RL DNA Res. 10:167-180(2003);
DR EMBL; AK129258; BAC98068.2; -;
DR InterPro; IPR001220; Lectin_legB.
DR Pfam; PF04054; Noct1; 1.
DR PROSITE; PS00307; LECTIN_LEGUME_BETA; UNKNOWN_1.
FT NON TER
SQ SEQUENCE 1458 AA; 165136 MW; 7752261AAA0BAFC9 CRC64;

Query Match 94.8%; Score 1178; DB 2; Length 1458;
Best Local Similarity 99.6%; Pred. No. 1.2e-93;
Matches 225; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 13 QVDMLEINIAPIRLNFTGWPMPQPKDLSYKTRSPVTLSDLRSLQVNEPGRNY 72
DB 1233 KVDMLSEINIAPIRLNFTGWPMPQPKDLSYKTRSPVTLSDLRSLQVNEPGRNY 1292
QY 73 NQOLINALVLYGTQAIHAIHNKGSTPSMSTITHSAMMDI FQNLAVDLDTGGYFLPLAI 132
DB 1293 NQOLINALVLYGTQAIHAIHNKGSTPSMSTITHSAMMDI FQNLAVDLDTGGYFLPLAI 1352
QY 133 ANQLRPNSHHTYFSCMTLYLFAEANTBAIQEQITVLLERLLVNRPHPGILLITFIELI 192
DB 1353 ANQLRPNSHHTYFSCMTLYLFAEANTBAIQEQITVLLERLLVNRPHPGILLITFIELI 1412
QY 193 KNPAPFKNHBFVHCAPBEIKL FQSVVACCMGCKQAOQVMEGTGAS 238
DB 1413 KNPAPFKNHBFVHCAPBEIKL FQSVVACCMGCKQAOQVMEGTGAS 1458

RESULT 5
Q8TB53 PRELIMINARY; PRT; 1620 AA.
AC Q8TB53;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE KIAA1007 protein (fragment).
GN Name=KIAA1007;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Uterus;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altshuler S.P., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Schetz T.E.,
RA Brownstein M.J., Ueda T.B., Toshikiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Muljady S.J.,
RA Bosak S.A., McMan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Huliy S.W.,
RA Villalón D.K., Muzny D.M., Sodergren J., Lu X., Gibbs R.A.,
RA Fehey J., Helton E., Ketterman M., Madan A., Rodriguez S., Sanchez A.,

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RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywicki M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Uterus;
RX Strausberg R.;
RA Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
RL EMBL; BC024317; AAH24317.1; -;
DR InterPro; IPR001220; Lectin_legB.
DR Pfam; PF04054; Noct1; 1.
DR PROSITE; PS00307; LECTIN_LEGUME_BETA; UNKNOWN_1.
FT NON TER
SQ SEQUENCE 1620 AA; 183241 MW; 6F59D887182E0A63 CRC64;

Query Match 94.8%; Score 1178; DB 2; Length 1620;
Best Local Similarity 99.6%; Pred. No. 1.4e-93;
Matches 225; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 13 QVDMLEINIAPIRLNFTGWPMPQPKDLSYKTRSPVTLSDLRSLQVNEPGRNY 72
DB 1395 KVDMLSEINIAPIRLNFTGWPMPQPKDLSYKTRSPVTLSDLRSLQVNEPGRNY 1454
QY 73 NQOLINALVLYGTQAIHAIHNKGSTPSMSTITHSAMMDI FQNLAVDLDTGGYFLPLAI 132
DB 1455 NQOLINALVLYGTQAIHAIHNKGSTPSMSTITHSAMMDI FQNLAVDLDTGGYFLPLAI 1514
QY 133 ANQLRPNSHHTYFSCMTLYLFAEANTBAIQEQITVLLERLLVNRPHPGILLITFIELI 192
DB 1515 ANQLRPNSHHTYFSCMTLYLFAEANTBAIQEQITVLLERLLVNRPHPGILLITFIELI 1574
QY 193 KNPAPFKNHBFVHCAPBEIKL FQSVVACCMGCKQAOQVMEGTGAS 238
DB 1575 KNPAPFKNHBFVHCAPBEIKL FQSVVACCMGCKQAOQVMEGTGAS 1620

RESULT 6
Q9T2L0 PRELIMINARY; PRT; 1635 AA.
AC Q9T2L0;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE KIAA1007 protein (fragment).
GN Name=KIAA1007;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=99246063; PubMed=10231032; Kikuno R., Hirogawa M.,
RA Nagase T., Ishikawa K., Suyama M., Kikuno R., Ohara O.,
RA Miyajima N., Tanaka A., Kotani H., Nomura N., Ohara O.;
RT "Prediction of the coding sequences of unidentified human genes. XIII.
RT for large proteins in vitro.";
RL DNA Res. 6:63-70(1999).
DR EMBL; AB023224; BAA76851.2; -;
DR InterPro; IPR001220; Lectin_legB.
DR Pfam; PF04054; Noct1; 1.
DR PROSITE; PS00307; LECTIN_LEGUME_BETA; UNKNOWN_1.
FT NON TER
SQ SEQUENCE 1835 AA; 206328 MW; BD9B12CE57A71175 CRC64;

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Query Match          94.8%; Score 1178; DB 2; Length 1835;
Best Local Similarity 99.6%; Pred. No. 1.6e-93;
Matches 225; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 13 QVDMSEINIARILTNFTGWPPOPKOLDYLKTRSPVTLSDLRSLQVSNFGRNY 72
   :|||||
Db 1610 KYDMSSEINIARILTNFTGWPPOPKOLDYLKTRSPVTLSDLRSLQVSNFGRNY 1669
   :|||||

QY 73 NQOLINALVYGTQAIHAIHNKSTSPSNTTSHAHMDIFQNLAVDLDTBGRYFLNMI 132
   :|||||
Db 1670 NQOLINALVYGTQAIHAIHNKSTSPSNTTSHAHMDIFQNLAVDLDTBGRYFLNMI 1729
   :|||||

QY 133 ANQLRYPNSHTYFSCITMLYFLPAEANTBAIOEQITRVLLERLIIVNRPHPMGLITITIELI 192
   :|||||
Db 1730 ANQLRYPNSHTYFSCITMLYFLPAEANTBAIOEQITRVLLERLIIVNRPHPMGLITITIELI 1789
   :|||||

QY 193 KNPAPKFMNHEFVHCAPETIEKLFQSVAAOCQMGOKAQOQWEGTGAS 238
   :|||||
Db 1790 KNPAPKFMNHEFVHCAPETIEKLFQSVAAOCQMGOKAQOQWEGTGAS 1835
   :|||||

RESULT 7
Q68DX7 PRELIMINARY; PRT; 2127 AA.
ID Q68DX7;
AC Q68DX7;
DT 25-OCT-2004 (TREMBLrel. 28, Created)
DT 25-OCT-2004 (TREMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TREMBLrel. 28, Last annotation update)
DE Hypothetical protein DKFZp686E0722.
GN Name=DKFZp686E0722;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Testis;
RG The German CDNA Consortium;
RA Poustka A., Albert R., Moosmayer P., Schnupp I., Wellenreuther R.,
RA Mewes H.W., Weill B., Amd C., Oeinger A., Fobio G., Han M., Wiemann S.;
RA Submitted (AUG-2004) to the EMBL/Genbank/DBJ databases.
RL EMBL; CR749237; CNI18093.1; -.
DR InterPro; IPR001220; Lectin_1egB.
DR InterPro; IPR007196; Lectin_1egB.
DR Pfam; PF04054; Noct1.1.
DR PROSITE; PS00307; LECTIN_LBGIME_BETA; UNKNOWN_1.
SQ SEQUENCE 2127 AA; 239113 MW; ABSDI92D6944037 CRC64;

Query Match          94.8%; Score 1178; DB 2; Length 2127;
Best Local Similarity 99.6%; Pred. No. 2e-93;
Matches 225; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 13 QVDMSEINIARILTNFTGWPPOPKOLDYLKTRSPVTLSDLRSLQVSNFGRNY 72
   :|||||
Db 1902 KYDMSSEINIARILTNFTGWPPOPKOLDYLKTRSPVTLSDLRSLQVSNFGRNY 1961
   :|||||

QY 73 NQOLINALVYGTQAIHAIHNKSTSPSNTTSHAHMDIFQNLAVDLDTBGRYFLNMI 132
   :|||||
Db 1962 NQOLINALVYGTQAIHAIHNKSTSPSNTTSHAHMDIFQNLAVDLDTBGRYFLNMI 2021
   :|||||

QY 133 ANQLRYPNSHTYFSCITMLYFLPAEANTBAIOEQITRVLLERLIIVNRPHPMGLITITIELI 192
   :|||||
Db 2022 ANQLRYPNSHTYFSCITMLYFLPAEANTBAIOEQITRVLLERLIIVNRPHPMGLITITIELI 2081
   :|||||

QY 193 KNPAPKFMNHEFVHCAPETIEKLFQSVAAOCQMGOKAQOQWEGTGAS 238
   :|||||
Db 2082 KNPAPKFMNHEFVHCAPETIEKLFQSVAAOCQMGOKAQOQWEGTGAS 2127
   :|||||

RESULT 8
Q6C0H2 PRELIMINARY; PRT; 381 AA.
ID Q6C0H2
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AC Q6C0H2;
DT 01-MAR-2003 (TREMBLrel. 23, Created)
DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE Mus musculus 13 days embryo male testis cDNA, RIKEN full-length
DE enriched library, clone:603041K04 product:ADRENAL GLAND PROTEIN AD-
DE 005 homolog.
GN Name=603041K04Rik;
OS Mus musculus (Mouse)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Testis;
RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA Carninci P., Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning.";
RL Meth. Enzymol. 303:19-44 (1999).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Testis;
RX MEDLINE=2108560; PubMed=11217851; DOI=10.1038/35055500;
RA RIKEN FANTOM Consortium;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690 (2001).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Testis;
RA The FANTOM Consortium,
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcription profile based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573 (2002).
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Testis;
RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA Komno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
RT prepare full-length cDNA libraries for rapid discovery of new genes.";
RL Genome Res. 10:1617-1630 (2000).
RN [5]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Testis;
RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA Komno H., Akiyama J., Nishi K., Kitsuana T., Tashiro H., Itoh M.,
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada K.,
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Watabiki M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system-384-format
RT sequencing pipeline with 384 multicapillary sequencer.";
RL Genome Res. 10:1757-1771 (2000).
RN [6]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Testis;
RA Adachi J., Aizawa K., Akiyama T., Arikawa T., Bono H., Carninci P.,
RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
RA Hayashida K., Hayatsu N., Hiramoto K., Hiroka T., Hirozane T.,
RA Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
RA Nishi K., Nomura K., Numazaki R., Ono M., Ohsato N., Okazaki Y.,
RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
RA Saeki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
RA Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
RA Tomaru A., Toyota T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
RL Submitted (JUL-2001) to the EMBL/Genbank/DBJ databases.
EMBL; AK031357; BAC27364.1; -.
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RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,  
 RA de Pablo B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,  
 RA Dodeon K., Doup L.B., Downes N., Dugan-Rocha S., Dunkov B.C., Dunn P.,  
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,  
 RA Foster C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,  
 RA Gloder A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,  
 RA Harris N.L., Harvey D., Heitman T.J., Hernandez J.B., Houck J.,  
 RA Heston D., Heston K.A., Howland T.J., Mei M.H., Ibegyan C.,  
 RA Jalali M., Kalush P., Karpen G.H., Ke Z., Kennison J.A., Kechum K.A.,  
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,  
 RA Laeko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,  
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,  
 RA Mekulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,  
 RA Mount S.R., Neeson K.A., Nixon K., Nusken D.R., Pacled J.M.,  
 RA Palazzolo M., Peltman G.S., Pan S., Pollard J., Puri V., Reese M.G.,  
 RA Reinert K., Remington K., Saunders R.D., Scheeler F., Shen H.,  
 RA Shue B.C., Siden-Klamos I., Simpson M., Skupski M.P., Smith T.,  
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,  
 RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,  
 RA Wang Z.Y., Wasserman D.A., Weinstein G.M., Weissbach J.,  
 RA Williams S.M., Woodgett, Worley K.C., Wu D., Yang S., Yao Q.A., Ye J.,  
 RA Yeh R.F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,  
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,  
 RA Gdbbs R.A., Myers B.W., Rubin G.M., Venter J.C.;  
 RT "The genome sequence of *Drosophila melanogaster*,"  
 RL Science 287:2185-2195(2000).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=22426065; PubMed=12537568;  
 RA Colinker S.E., Wheeler D.A., Krommiller B., Carlson J.W., Halpern A.,  
 RA Patel S., Adams M., Champe M., Dugan S.P., Fribe E., Nelson C.R.,  
 RA George R.A., Hoskins R.A., Laverly T., Muzny D.M., Nelson C.R.,  
 RA Pacled J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J.,  
 RA Svirskas R., Taber P.E., Wan K., Stapleton M., Sutton G.G., Venter C.,  
 RA Weinstein G., Scherer S.E., Myers B.W., Gdbbs R.A., Rubin G.M.;  
 RT "Finishing a whole-genome shotgun: Release 3 of the *Drosophila*  
 RT melanogaster euchromatic genome sequence,"  
 RL Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=22426070; PubMed=12537573;  
 RA Kaminker J.S., Bergman C.M., Krommiller B., Carlson J., Svirskas R.,  
 RA Patel S., Fribe E., Wheeler D.A., Lewis S.E., Rubin G.M.,  
 RA Ashburner M., Colinker S.E.;  
 RT "The transposable elements of the *Drosophila melanogaster* euchromatin:  
 RT a genomics perspective,"  
 RL Genome Biol. 3:RESEARCH0084-RESEARCH0084(2002).  
 RN [4]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=22426069; PubMed=12537572;  
 RA Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,  
 RA Hradecky P., Huang Y., Kaminker J.S., Milburn G.H., Prochuk S.B.,  
 RA Smith C.D., Tupy J.L., Whitfield J.D., Bayraktaroglu I., Berman B.P.,  
 RA Bettecourt B.R., Colinker S.E., de Grey A.D., Drysdale R.A.,  
 RA Harris N.L., Richter C., Russo S., Schroeder A.J., Shu S.Q.,  
 RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,  
 RA Lewis S.E.;  
 RT "Annotation of the *Drosophila melanogaster* euchromatic genome: a  
 RT systematic review,"  
 RL Genome Biol. 3:RESEARCH0083-RESEARCH0083(2002).  
 RN [5]  
 RP SEQUENCE FROM N.A.  
 RG FlyBase;  
 RN Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.  
 RP [6]  
 RP SEQUENCE FROM N.A.  
 RG FlyBase;  
 RN Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AEO03833; AAM71069.2; -  
 DR FlyBase; FBgn0033424; CG1884.  
 DR InterPro; IPR000577; FGGY kin.  
 DR InterPro; IPR003006; Ig\_MHC.

DR InterPro; IPR001220; Lectin\_1egb.  
 DR InterPro; IPR007196; Nocl.  
 DR Pfam; PF04054; Nocl. 1.  
 DR PROSITE; PS00445; FGGY\_KINASES\_2; UNKNOWN\_1.  
 DR PROSITE; PS00290; IG\_MHC; UNKNOWN\_1.  
 DR PROSITE; PS00307; LECTIN\_LEGUME\_BETA; UNKNOWN\_1.  
 SO SEQUENCE 2172 AA, 244235 MW, 48B008684EB79CCF CRC64;  
 Query Match 70.24; Score 873; DB 2; Length 2172;  
 Best Local Similarity 71.74; Pred. No. 7.9e-67;  
 Matches 165; Conservative 30; Mismatches 29; Indels 6; Gaps 2;  
 Oy 13 QVWLSRINAPILLTNF-TGVWPGKQDLSYTKRSVTLSDRSNLQVSEKGR 71  
 Db 1936 KVDLSSNAFVPLSSVLIWNIQIPANKKQDLSYTKRRAVTLSELGHLQVTSKGR 1995  
 Oy 72 YNQLIALVLYGTQAIHAIHNKSGSPSSMTTSHAMDI FQNLAVDLTDEGRYLP 131  
 Db 1996 YNMAKMAVLYGTQAIHAIHNKSGSPSSMTTSHAMDI FQNLAVDLTDEGRYLP 2055  
 Oy 132 IANQLRPNSTHYFSCMLYLPFAEANTAEIQOITRVLLERLI VNRPHPGILLITFBL 191  
 Db 2056 IANQLRPNSTHYFSCAVLHLPFAEANSSEAIQOITRVLLERLI VNRPHPGILLITFBL 2115  
 Oy 192 IKNPAPFPMNHEFVHCAPETIKLPGSVACCMQKQAO-----VNEGTG 236  
 Db 2116 IKNPYFMDHDFVHCAPETIKLPGSVARSCLAKSVNTQOLNMPVVDGEG 2165  
 RESULT 13  
 ID Q8BXB2 PRELIMINARY; PRT; 424 AA.  
 AC Q8BXB2;  
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)  
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)  
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
 DE Mus musculus 16 days embryo head cDNA, RIKEN full-length enriched  
 DE library, clone:c130038P19 product:ADRENAL GLAND PROTEIN AD-005  
 DE homolog.  
 GN Name=603041K04R1k;  
 OS Mus musculus (Mouse)  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6J; TISSUE=Head;  
 RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6679(99)03004-9;  
 RA Carminec P., Hayaishizeki Y.;  
 RT "High-efficiency full-length cDNA cloning,"  
 RL Meth. Enzymol. 303:19-44(1999).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6J; TISSUE=Head;  
 RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;  
 RA RIKEN FANTOM Consortium;  
 RT "Functional annotation of a full-length mouse cDNA collection,"  
 RL Nature 409:685-690(2001).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6J; TISSUE=Head;  
 RA The FANTOM Consortium;  
 RT "The RIKEN Genome Exploration Research Group Phase I & II Team;  
 RT "Analysis of the mouse transcriptome based on functional annotation of  
 RT 60,770 full-length cDNAs,"  
 RL Nature 420:563-573 (2002).  
 RN [4]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6J; TISSUE=Head;  
 RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/9r.145100;  
 RA Carminec P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,  
 RA Komori H., Okazaki Y., Muramatsu M., Hayaishizeki Y.;  
 RT "Normalization and subtraction of cap-trapper-selected cDNAs to

[illegible]

RG WormBase Consortium;  
RT "Genome sequence of the nematode *C. elegans*: a platform  
RT investigating biology, the *C. elegans* Sequencing Consort  
RL Science 282:2012-2018 (1998) .  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=Bristol N2;  
RA Pavello A.;  
RT "The sequence of *C. elegans* cosmid F57B9.";  
RL Submitted (NOV-1994) to the EMBL/GenBank/DBJ databases.  
RN [3]  
RP SEQUENCE FROM N.A.  
RC STRAIN=Bristol N2;  
RA Waterston R.;  
RL Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.  
RN [4]  
RP SEQUENCE FROM N.A.  
RC STRAIN=Bristol N2;  
RA Wilson R.;  
RL Submitted (APR-2004) to the EMBL/GenBank/DBJ databases.  
RN [5]  
RP SEQUENCE FROM N.A.  
RC STRAIN=Bristol N2;  
RG WormBase Consortium;  
RL Submitted (SEP-2004) to the EMBL/GenBank/DBJ databases.  
RL EMBL, U13876; AAA21168.1; -.  
DR PIR, G88493; G88493.  
DR WormBase; WBGene00003824; ncl-1.  
DR WormPep; F57B9.2; CE01337.  
DR InterPro; IPR001547; Glyco\_hydro\_5.  
DR InterPro; IPR007196; Nccl1.  
DR Pfam; PF04054; Nccl1.1.  
DR PROSITE; PS00659; GLYCOSYL\_HYDROL\_F5; UNKNOWN1.  
SQ SEQUENCE 2500 AA; 278990 MW; 055808606FF56975 CRC64;

Query	March	52.5%	Score 653	DB 2	Length 2500
Best local similarity	53.8%	Pred. No. 1.4e-47			
Matches 121	Conservative 34	Mismatches 70	Indels 0	Gaps 0	

  

Qy	13	QVDMLSBINIAFRILITNFTGVPDQFKKDDLSYKTRSPYFSLDRLSNLQVNSPEGRY	72
Db	2256	QVDTITPEMAVPEKSNLMNATITIPNIRIPDEYLANRISVDFPNLPITLQTONOAGTKY	2315
Qy	73	NLOILNLTLYVYGQATAHINKGSTPSMTSTHSAMDIFONLAVLDTEGRYLFNAI	132
Db	2316	NTYWNALVTVGFRALIEHLRLRQISTNIAHSTSYNDIFONALIQDITGRYLFNGI	2375
Qy	133	ANQLRYPNSHTHTYSCETMLYFAEANTAEIOEQITRVLLERLIYNRPHPMGLITFIELI	192
Db	2376	ANQLRYPNANHHTYSCVFLYFKNSTMDTIOEQITRILFELVLNRPHPMGLITFIELI	2433
Qy	193	KNPAPKFNHNEFVHCAPRIEKLFPQSVAAQCCMGQKQAOQVMEGTG	237
Db	2436	KNPTYNFWRVYEFSCAPEIQRLPQNVANTCVPAQSGQPOAPDGA	2480

  

RESULT 15	Q94LQ9	PRELIMINARY;	PRT;	2363 AA.
ID	Q94LQ9			
AC	Q94LQ9; Q7XC99;			
DT	01-DEC-2001 (TREMBLrel. 19, Created)			
DT	01-DEC-2001 (TREMBLrel. 19, Last sequence update)			
DT	05-JUL-2004 (TREMBLrel. 27, Last annotation update)			
DE	Putative transcription regulatory protein.			
GN	ORFNames=OSUNBa0010C11.3;			
OS	Oryza sativa (japonica cultivar-group) .			
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;			
OC	Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;			
OC	Ehrhartoideae; Oryzeae; Oryza.			
CC				
NCBI	NCBI_TaxId=39947;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RA	Buell C.R., Yuan Q., Ouyang S., Moffat K.S., Hill J.N., Gansberger K.,			

RA Brenner M., Burgess S., Hance M., Shvartsbeyn M., Taitlin T.,  
 RA Riggs F., Hsiao J., Ziemann V., Blunt S., Pal G., Vanaken S.B.,  
 RA Utechtack T.R., Feldblyum T.V., Quackenbush J., Salzberg S.L.,  
 RA White O., Fraser C.M.,  
 RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RA Buell R.,  
 RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RA The Rice Chromosome 10 Sequencing Consortium;  
 RT "In-depth view of structure, activity, and evolution of rice  
 RT chromosome 10.",  
 RL Science 300:1566-1569(2003).  
 RN [4]  
 RP SEQUENCE FROM N.A.  
 RA Buell C.R., Ming R.A., McComble W.R., Messing J., Yuan Q.,  
 RL Submitted (MAY-2003) to the EMBL/GenBank/DBJ databases.  
 DR EMBL/AC069300; AAK55455.1; -.  
 DR EMBL/AB017118; AAP54975.1; -.  
 DR Gramene; Q7XC99; -.  
 DR Gramene; Q94IQ9; -.  
 DR InterPro; IPR007196; Noct1.  
 DR Pfam; PF04054; Noct1; 1.  
 SQ SEQUENCE 2363 AA; 262004 MW; 2AB523628FCA875C CRC64;

Query Match 50.0%; Score 621.5; DB 2; Length 2363;  
 Best Local Similarity 55.1%; Pred. No. 7.5e-45;  
 Matches 125; Conservative 38; Mismatches 49; Indels 15; Gaps 5;

QY 13 QVMSLSINIAPIRLTPTGVN-PPQPKOLDSTLKTSPVTFPSDLSNLQV---SNR 67  
 DB 2125 KIDLAEISIPRIMSDVDALSKQWKTVDEYTK-RPDGSFYTDLKQKLLLPQNEANI 2183  
 QY 68 PGRVYNQLINALVLYVGTQAIHIN-KGSTPEMSTITSAHMDI-----FQNLAV 118  
 DB 2184 AGTRINPLVNSLVYGMQVQOLQNKMAASASAOQMQSOLVDQIETATETELFRNLVM 2243  
 QY 119 DLDTEGRYLPFLNAINQRLRYPNSHTHYFSCMTLYLPAEANTKAIQEQITRVLLERLIVNR 178  
 DB 2244 NSDTEGRYLLNAINQRLRYPNNHHTHYFSPILYLPSEANQEIQEQITRVLLERLIVNR 2303  
 QY 179 PHPWGLITITIELIKNPAFKFNHFFVCAPEIEKLFQSYAQCQMGQ 225  
 DB 2304 PHPWGLITITIELIKNPRVGFMAKSPTRCAPEIEKLFESVARSCGK 2350

Search completed: July 14, 2005, 20:32:01  
 Job time : 83.5891 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: July 14, 2005, 19:54:41 ; Search time 105.417 Seconds

(without alignments)  
1196.043 Million cell updates/sec

Title: US-10-019-151C-3

Perfect score: 1738  
Sequence: 1 MARVELSKARSGQRTLLSAT.....RGASQELKAVRSVVEEQC 326

Scoring table: BIOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

A\_Geneseq\_16Dec04:\*  
1: geneseqp1980s:\*  
2: geneseqp1980s:\*  
3: geneseqp2000s:\*  
4: geneseqp2001s:\*  
5: geneseqp2002s:\*  
6: geneseqp2003as:\*  
7: geneseqp2003bs:\*  
8: geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1738	100.0	326	4 AAB20091	Aab20091 Human hyd
2	1733	99.7	326	4 AAM93915	Aam93915 Human pol
3	1733	99.7	326	8 ADL32038	ADL32038 Human pro
4	1725	99.3	339	2 AAY29331	Aay29331 Human sec
5	1725	99.3	339	4 AAU39057	AAU39057 Human sec
6	1725	99.3	339	5 ABB55766	ABB55766 Human pol
7	1450.5	83.5	275	4 AAM93907	Aam93907 Human pol
8	1450.5	83.5	275	8 ADL32022	ADL32022 Human pro
9	1232	70.9	323	6 ABJ19723	ABJ19723 Human sec
10	1232	70.9	323	6 ABP99774	ABP99774 Human sec
11	1232	70.9	323	6 ABR01267	ABR01267 Human gen
12	1232	70.9	323	6 ADA98352	ADA98352 Human sec
13	1232	70.9	324	3 AAB51635	Aab51635 Human sec
14	1086	62.5	330	5 ABB88807	ABB88807 Human pol
15	987.5	56.8	343	4 AAM93674	Aam93674 Human pol
16	987.5	56.8	343	8 ADL31529	ADL31529 Human pro
17	887.5	51.1	304	6 ADA14417	ADA14417 Mouse spe
18	669.5	38.5	357	5 ABB97772	ABB97772 Human sec
19	669.5	38.5	359	6 ABB75926	ABB75926 Human sec
20	669.5	38.5	359	6 ABB75926	ABB75926 Human sec
21	657.5	37.8	285	3 AAY66710	Aay66710 Membrane
22	657.5	37.8	285	4 AAU12395	AAU12395 Human PRO
23	657.5	37.8	285	4 AAB94851	Aab94851 Human PRO
24	657.5	37.8	285	4 AAB65233	Aab65233 Human PRO
25	657.5	37.8	285	6 ABUS8048	Abus8048 Human PRO

26	657.5	37.8	285	6 ABUS9126	Abus9126 Novel hum
27	657.5	37.8	285	6 ABUS2638	Abus2638 Human sec
28	657.5	37.8	285	6 AB017839	Ab017839 Novel hum
29	657.5	37.8	285	6 ABUS0557	Abus0557 Human sec
30	657.5	37.8	285	6 ABUS13939	Abus13939 Human PRO
31	657.5	37.8	285	6 ABUS1093	Abus1093 Human PRO
32	657.5	37.8	285	6 ABUS72524	Abus72524 Novel hum
33	657.5	37.8	285	6 ABUS6793	Abus6793 Human PRO
34	657.5	37.8	285	6 ABUS9874	Abus9874 Novel sec
35	657.5	37.8	285	6 ABUS9273	Abus9273 Human sec
36	657.5	37.8	285	6 ABO25970	Ab025970 Human PRO
37	657.5	37.8	285	6 ABO25064	Ab025064 Human sec
38	657.5	37.8	285	6 ABUS8979	Abus8979 Human sec
39	657.5	37.8	285	6 ABUS92357	Abus92357 Novel hum
40	657.5	37.8	285	6 ABUS9422	Abus9422 Novel hum
41	657.5	37.8	285	6 ABUS7069	Abus7069 Human sec
42	657.5	37.8	285	6 ABUS2188	Abus2188 Novel hum
43	657.5	37.8	285	6 ABUS10894	Abus10894 Human PRO
44	657.5	37.8	285	6 ABUS1646	Abus1646 Novel hum
45	657.5	37.8	285	6 ABUS8585	Abus8585 Human sec

#### ALIGNMENTS

RESULT 1  
AAB20091  
ID AAB20091 standard; protein; 326 AA.

AC AAB20091;

DT 23-APR-2001 (first entry)

DE Human hydrophobic domain-containing protein HP03371.

XX Human; hydrophobic domain; antiinflammatory; immunosuppressive;

XX immunostimulant; vulnery; antilucer; haemostatic; cytotoxic;

KW hepatotropic; thrombolytic; antitumour; antiviral; antibacterial;

XX antifungal; gene therapy; diagnosis; membrane protein.

XX Homo sapiens.

PN WC0200100824-A2.

PF 16-JUN-2000; 2000WO-JP003944.

PR 24-JUN-1999; 99JP-00178065.

PA (SAGA) SAGAMI CHEM RES CENT.

XX (PROT-) PROTEGENE INC.

PI Kato S, Kimura T;

XX WPI, 2001-123008/13.

DR N-PSDB; AAB20091.

PT New proteins with hydrophobic domains, useful for treating autoimmune

XX diseases, inflammatory diseases, wounds, burns, incisions and ulcers.

PS Claim 1, Page 89-90; 126pp; English.

The present sequence is that of a novel human protein having 2 putative  
transmembrane domains. It is predicted from cDNA clone HP03371 (see  
AF030022), isolated from a lymphoma cell line U937 cDNA library. The  
predicted 39 kDa protein shows 71.5% homology to mouse protein GSG1. The  
invention provides human proteins (see AAB20089-96) having hydrophobic  
domains indicative of secretory signals or membrane domains, and nucleic  
acids (see AAF30020-27) encoding them. These are expected to have cell  
proliferation, cell differentiation, immunostimulant or immunosuppressor,  
chemotaxis, haemostatic, tissue growth, activin, inhibin, chemotactic,  
chemokinetic, haemostatic, thrombolytic, receptor/ligand.

CC antiinflammatory or antitumour activities (no evidence provided).  
 CC Expression vectors, eukaryotic host cells and antibodies are also  
 CC provided. The secreted or membrane proteins of the invention can be used  
 CC as pharmaceuticals or antigens for preparing antibodies. Cells expressing  
 CC them are utilized for detection of corresponding receptors or ligands,  
 CC and in candidate drug screening

XX  
 SQ Sequence 326 AA;

Query Match 100.0%; Score 1738; DB 4; Length 326;  
 Best Local Similarity 100.0%; Pred. No. 1.7e-175;  
 Matches 326; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAKMEISKAFSGQRTILSLISLMSLSFTTSLSNYPVGTQKPKPLCEKGLAAKCPD 60  
 DB 1 MAKMEISKAFSGQRTILSLISLMSLSFTTSLSNYPVGTQKPKPLCEKGLAAKCPD 60  
 QY 61 MPVSLDGDNTSTQEVQYNMETGDDRFSPFRSGMWLSCETVEEPGERCRSFTELTP 120  
 DB 61 MPVSLDGDNTSTQEVQYNMETGDDRFSPFRSGMWLSCETVEEPGERCRSFTELTP 120  
 QY 121 PAKREILMLSLGTQITTYIGLQFISFLLLTDLITGNPACGLKLSAFAVSSVLSGLLGM 180  
 DB 121 PAKREILMLSLGTQITTYIGLQFISFLLLTDLITGNPACGLKLSAFAVSSVLSGLLGM 180  
 QY 181 VAHMYTSQVFOATVNLGPEDMRPHVMNYGMAFYMAWLSFTCCMASAVTTENTYTRMULEF 240  
 DB 181 VAHMYTSQVFOATVNLGPEDMRPHVMNYGMAFYMAWLSFTCCMASAVTTENTYTRMULEF 240  
 QY 241 KCKHSKSPKENPNCPLPHHQCPRRLSSAAPTGVGLTSTYHQYNQPIHSVSEGVDFYSEL 300  
 DB 241 KCKHSKSPKENPNCPLPHHQCPRRLSSAAPTGVGLTSTYHQYNQPIHSVSEGVDFYSEL 300  
 QY 301 RNKGFORGASQELKEAVRSSVEEEQC 326  
 DB 301 RNKGFORGASQELKEAVRSSVEEEQC 326

RESULT 2  
 AAM93915  
 ID AAM93915 standard; protein; 326 AA.

XX AAM93915;  
 AC AAM93915;  
 DT 06-NOV-2001 (first entry)  
 XX Human polypeptide, SEQ ID NO: 4071.  
 KW Human; full length cDNA; cDNA synthesis; oligo-capping.  
 XX Homo sapiens.  
 OS Homo sapiens.  
 PN EP130094-A2.  
 PD 05-SEP-2001.  
 XX 07-JUL-2000; 2000EP-00114089.  
 PF 08-JUL-1999; 99JP-00194486.  
 PR 11-JAN-2000; 2000JP-00118774.  
 PR 02-MAY-2000; 2000JP-00183765.  
 XX (HELI-) HELIX RES INST.

PI Ota T, Nishikawa T, Isogai T, Hayashi K, Ishii S, Kawai Y;  
 PI Wakamatsu A, Sugiyama T, Nagai K, Kojima S, Otsuki T, Koga H;  
 DR WPI; 2001-524255/58.  
 DR N-PSDB; AAK94877.  
 PT 830 Primers useful for synthesizing full length cDNA clones and their use  
 PT in genetic manipulation.  
 XX

PS Claim 8; SEQ ID NO 4071; 1380bp + Sequence Listing; English.

XX The invention relates to primers for synthesizing full length cDNA  
 CC clones. 830 cDNA molecules encoding a human protein have been isolated  
 CC and nucleotide sequences of 5'- and 3'-ends of the cDNA molecules have  
 CC been determined. Primers for synthesizing the full length cDNA are useful  
 CC for clarifying the function of the protein encoded by the cDNA. The full  
 CC length clones were obtained by construction of full length enriched cDNA  
 CC libraries that were synthesised by the oligo-capping method. The primers  
 CC enable the production of the full length cDNA easily without any special  
 CC methods. The present sequence is a polypeptide encoded by a full length  
 CC human cDNA of the invention. Note: The sequence data for this patent did  
 CC not form part of the printed specification, but was obtained in CD-ROM  
 CC format directly from EPO

XX  
 SQ Sequence 326 AA;

Query Match 99.7%; Score 1733; DB 4; Length 326;  
 Best Local Similarity 99.7%; Pred. No. 5.9e-175;  
 Matches 325; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MAKMEISKAFSGQRTILSLISLMSLSFTTSLSNYPVGTQKPKPLCEKGLAAKCPD 60  
 DB 1 MAKMEISKAFSGQRTILSLISLMSLSFTTSLSNYPVGTQKPKPLCEKGLAAKCPD 60  
 QY 61 MPVSLDGDNTSTQEVQYNMETGDDRFSPFRSGMWLSCETVEEPGERCRSFTELTP 120  
 DB 61 MPVSLDGDNTSTQEVQYNMETGDDRFSPFRSGMWLSCETVEEPGERCRSFTELTP 120  
 QY 121 PAKREILMLSLGTQITTYIGLQFISFLLLTDLITGNPACGLKLSAFAVSSVLSGLLGM 180  
 DB 121 PAKREILMLSLGTQITTYIGLQFISFLLLTDLITGNPACGLKLSAFAVSSVLSGLLGM 180  
 QY 181 VAHMYTSQVFOATVNLGPEDMRPHVMNYGMAFYMAWLSFTCCMASAVTTENTYTRMULEF 240  
 DB 181 VAHMYTSQVFOATVNLGPEDMRPHVMNYGMAFYMAWLSFTCCMASAVTTENTYTRMULEF 240  
 QY 241 KCKHSKSPKENPNCPLPHHQCPRRLSSAAPTGVGLTSTYHQYNQPIHSVSEGVDFYSEL 300  
 DB 241 KCKHSKSPKENPNCPLPHHQCPRRLSSAAPTGVGLTSTYHQYNQPIHSVSEGVDFYSEL 300  
 QY 301 RNKGFORGASQELKEAVRSSVEEEQC 326  
 DB 301 RNKGFORGASQELKEAVRSSVEEEQC 326

RESULT 3  
 ADL32038  
 ID ADL32038 standard; protein; 326 AA.

XX ADL32038;  
 AC ADL32038;  
 DT 20-MAY-2004 (first entry)  
 XX Human protein encoded by a full length cDNA clone segID 4071.  
 DE Human protein encoded by a full length cDNA clone segID 4071.  
 KW human; medicine; signal transduction; glycoprotein; transcription;  
 XX oligo-capping method.  
 OS Homo sapiens.  
 OS Homo sapiens.  
 PN EP1396543-A2.  
 PD 10-MAR-2004.  
 XX 07-JUL-2000; 2003EP-00025638.  
 PF 08-JUL-1999; 99JP-00194486.  
 PR 11-JAN-2000; 2000JP-00118774.  
 PR 02-MAY-2000; 2000JP-00183865.  
 PR 07-JUL-2000; 2000EP-00114089.  
 XX (REAS-) RES ASSOC BIOTECHNOLOGY.

```

XX Ora T, Nishikawa T, Isogai T, Hayashi K, Ichii S, Kawai Y;
PI Makamatsu A, Sugiyama T, Nagai K, Kojima S, Otsuki T, Koga H;
XX WPI; 2004-204755/20.
DR N-PSDB; ADL32037.
XX
PT New oligonucleotide primers (830 cDNAs) useful for synthesizing full
length human cDNAs.
XX
PS Example 1; SEQ ID NO 4071; 1340bp; English.
XX
CC This invention relates to a novel primers useful for synthesizing full
CC length cDNA molecules that encode human proteins. Specifically, it refers
CC to secretory or membrane proteins that are potential therapeutic agents/
CC target molecules in the field of medicine, and in particular genes
CC encoding proteins that are associated with signal transduction,
CC glycoproteins and transcription. The present invention describes a method
CC for efficiently cloning a full length human cDNA from both the 5' and 3'
CC ends using the oligo-capping method. This polypeptide sequence is a full
CC length human protein of the invention.
XX
SQ Sequence 326 AA;
Query Match 99.7%; Score 1733; DB 8; Length 326;
Best Local Similarity 99.7%; Pred. No. 5.9e-175;
Matches 325; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 MAKMEISKAFFSGQRTLLSAILSMLSLSTSTSLSNYPVGTQVPRPLCEKGLAAKCPD 60
DB 1 MAKMEISKAFFSGQRTLLSAILSMLSLSTSTSLSNYPVGTQVPRPLCEKGLAAKCPD 60
QY 61 MPVSLDDTNTSTQGVVQYNNMETGDDRRSPFRSGMWLSCETVBEGRCRSFIELTP 120
DB 61 MPVSLDDTNTSTQGVVQYNNMETGDDRRSPFRSGMWLSCETVBEGRCRSFIELTP 120
QY 121 PARREILMLSLGTQITTYIGLOFISFLLLTDLLLTGNPACGLKLSAFAAVSSVLSGLGM 180
DB 121 PARREILMLSLGTQITTYIGLOFISFLLLTDLLLTGNPACGLKLSAFAAVSSVLSGLGM 180
QY 181 VAHMTSQVFOATVNLGPEDMRPHVMYNGAFYMAVLSFTCMASAVTTFTNTYRMVLEF 240
DB 181 VAHMTSQVFOATVNLGPEDMRPHVMYNGAFYMAVLSFTCMASAVTTFTNTYRMVLEF 240
QY 241 KCHHSKSPKPNPCLPHHQCFFPRRLSSAAPTVGELTSTYQYHNPPIHSVSEGVDFYSEL 300
DB 241 KCHHSKSPKPNPCLPHHQCFFPRRLSSAAPTVGELTSTYQYHNPPIHSVSEGVDFYSEL 300
QY 301 RNKGFGASQELKEAVRSSVBEBOC 326
DB 301 RNKGFGASQELKEAVRSSVBEBOC 326
RESULT 4
AA29331
ID AA29331 standard; protein; 339 AA.
XX
AC AA29331;
XX
DT 29-SEP-1999 (first entry)
XX
DE Human secreted protein clone mt24_2 protein sequence.
XX
KW Human; secreted protein; nutrition; cytokine; cell proliferation;
KW differentiation; immune stimulating; vaccine; suppression; gene therapy;
KW haematopoiesis; immune growth; activin; inhibin; cadherin;
KW chemotactic; chemokinetic; haemostatic; thrombolytic; anti-inflammatory;
KW tumour invasion suppressor; tumour inhibition.
XX
OS Homo sapiens.
XX
AC AA29331;
XX
DT 29-SEP-1999 (first entry)
XX

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PD 29-JUL-1999.
XX
XX 21-JAN-1999; 99MO-US001404.
XX
XX 22-JAN-1998; 98US-0072134P.
XX
XX 20-JAN-1999; 99US-00235609.
XX
XX (GENMY ) GENETICS INST INC.
XX
XX Jacobs K, McCoy JM, Lavallie ER, Collins-Racie LA, Merberg D,
PI Treacy M, Agostino MJ, Steininger RJ, Wong GG, Clark HF, Reichel K,
XX
XX WPI; 1999-458682/38.
XX
DR N-PSDB; AAX90446.
XX
PT New polynucleotides encoding secreted human proteins derived from, e.g.
PT fetal brain potentially used as immunostimulators.
XX
PS Claim 28; Page 122-123; 139pp; English.
XX
CC The present sequence represents a human secreted protein. Human secreted
CC protein polynucleotides and proteins are predicted to have biological
CC activities which would make them suitable for treating, preventing or
CC ameliorating medical conditions in humans and animals, although no
CC supporting data is given. Suggested activities include nutritional
CC activity, cytokine and cell proliferation/differentiation activity,
CC immune stimulating (e.g. as vaccines) or suppressing activity,
CC haematopoiesis regulating activity, tissue growth activity,
CC activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic
CC and thrombolytic activity, receptor/ligand activity, anti-inflammatory
CC activity, cadherin/tumour invasion suppressor activity, and tumour
CC inhibition activity. The polynucleotides are also suited to be useful for
CC gene therapy.
XX
SQ Sequence 339 AA;
Query Match 99.3%; Score 1725; DB 2; Length 339;
Best Local Similarity 99.7%; Pred. No. 4.4e-174;
Matches 323; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 3 KHELSKAFSGQRTLLSAILSMLSLSTSTSLSNYPVGTQVPRPLCEKGLAAKCPD 62
DB 16 KHELSKAFSGQRTLLSAILSMLSLSTSTSLSNYPVGTQVPRPLCEKGLAAKCPD 62
QY 63 VSLDGDNTSTQGVVQYNNMETGDDRRSPFRSGMWLSCETVBEGRCRSFIELTPPA 122
DB 76 VSLDGDNTSTQGVVQYNNMETGDDRRSPFRSGMWLSCETVBEGRCRSFIELTPPA 122
QY 123 KREILMLSLGTQITTYIGLOFISFLLLTDLLLTGNPACGLKLSAFAAVSSVLSGLGMVA 182
DB 136 KREILMLSLGTQITTYIGLOFISFLLLTDLLLTGNPACGLKLSAFAAVSSVLSGLGMVA 182
QY 183 HMYYSQVFOATVNLGPEDMRPHVMYNGAFYMAVLSFTCMASAVTTFTNTYRMVLEFK 242
DB 196 HMYYSQVFOATVNLGPEDMRPHVMYNGAFYMAVLSFTCMASAVTTFTNTYRMVLEFK 242
QY 243 KHSKSPKPNPCLPHHQCFFPRRLSSAAPTVGELTSTYQYHNPPIHSVSEGVDFYSEL 302
DB 256 KHSKSPKPNPCLPHHQCFFPRRLSSAAPTVGELTSTYQYHNPPIHSVSEGVDFYSEL 302
QY 303 KGFQFGASQELKEAVRSSVBEBOC 326
DB 316 KGFQFGASQELKEAVRSSVBEBOC 339
RESULT 5
AAU39057
ID AAU39057 standard; protein; 339 AA.
XX
AC AAU39057;
XX
DT 16-JAN-2002 (first entry)
XX

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PA (AGOS/) AGOSTINO M J.  
 PA (STEL/) STEININGER R J.  
 PA (SPAU/) SPAULDING V.  
 PA (WONG/) WONG G G.  
 PA (CLAR/) CLARK H.  
 PA (FECH/) FECHTEL K.  
 XX  
 PI Jacobs K, McCoy JM, Lavallie ER, Collins-Racie LA, Evans C,  
 PI Merberg D, Treacy M, Agostino MJ, Steininger R, Spaulding V,  
 PI Wong GG, Clark H, Fechtel K,  
 DR WPI; 2002-040725/05.  
 DR N-PSDB; ABA90944.  
 XX  
 PT New secreted proteins and encoding polynucleotides, useful in gene  
 PT therapies, particularly for preventing or treating autoimmune disorders,  
 PT cancer, graft-versus-host disease, wound, osteoporosis, stroke or  
 PT inflammations.  
 XX  
 PS Disclosure; Page 276-277; 349pp; English.  
 CC The invention relates to isolated polynucleotides (ABA90876-ABA90968 and  
 CC ABA90980) and encoded proteins (AB55698-AB55800), especially  
 CC polynucleotides SEQ ID NO 1 (ABA90876) and SEQ ID NO 19 (ABA90885) and  
 CC proteins SEQ ID NO 2 (AB55698) and SEQ ID NO 20 (AB55707) contained in  
 CC clones bd306-7 and yb8-1 respectively and the clones bd306-7 and yb8-1  
 CC are deposited with the American Type Culture Collection (ATCC) with  
 CC accession number 98599. The polynucleotides and encoded polypeptides have  
 CC cytoprotective, anti-inflammatory, immunomodulator, vascular, thrombolytic  
 CC neuroprotective, activin, inhibin, chemotactic, hematopoietic, and  
 CC and anti-inflammatory activity and acting as cytokine modulators,  
 CC hemopoietic regulators, tissue growth modulators and/or cadherin  
 CC suppressors. The polypeptides and polynucleotides are useful in gene  
 CC therapies, particularly for preventing, treating or ameliorating any of  
 CC the following diseases: immune deficiency and disorders; e.g. bacterial  
 CC or fungal infections, autoimmune disorders; cancer, systemic lupus  
 CC erythematosus or graft-versus-host disease; myeloid or lymphoid cell  
 CC deficiencies; wound, burns, incisions and ulcers, osteoporosis or  
 CC osteoarthritis; central and peripheral nervous system diseases and  
 CC neuropathies; e.g. Alzheimer's, Parkinson's disease, Huntington's  
 CC disease, amyotrophic lateral sclerosis or Shy-Drager syndrome;  
 CC hemophilia, cardiac infarction or stroke; inflammations, shock, sepsis  
 CC or systemic inflammatory response syndrome, ischemia-reperfusion injury,  
 CC endotoxin lethality, arthritis, inflammatory bowel disease or Crohn's  
 CC disease; or tumours or cancers, pemphigus vulgaris or pemphigus foliaceus  
 CC  
 XX Sequence 339 AA;  
 SQ  
 Query Match 99.3%; Score 1725; DB 5; Length 339;  
 Best Local Similarity 99.7%; Pred. No. 4.4e-174;  
 Matches 323; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 3 KHELAKAFSGQRTLLSLNLSLSTSTSLSNYFVGQKPKPLCEKGLAKCPDM 62  
 DB 16 EMLSKAFSGQRTLLSLNLSLSTSTSLSNYFVGQKPKPLCEKGLAKCPDM 75  
 QY 63 VSLDGTNTSTQEVVQNMETGDRFGRSFRSGMWSCEETVEEPEGRCSFIELTPA 122  
 DB 76 VSLDGTNTSTQEVVQNMETGDRFGRSFRSGMWSCEETVEEPEGRCSFIELTPA 135  
 QY 123 KRELILWLSLGTQITTYIGLQPLISFLILLTDLTGPNPAGKLSAPAAVSSVLSGLGMVA 182  
 DB 136 KRELILWLSLGTQITTYIGLQPLISFLILLTDLTGPNPAGKLSAPAAVSSVLSGLGMVA 195  
 QY 183 HMMYSGVFOATVNLGPEDEMRPHVWNYGMAYMMLSTCCMAASAVTTFTNTYTRVLEFKC 242  
 DB 196 HMMYSGVFOATVNLGPEDEMRPHVWNYGMAYMMLSTCCMAASAVTTFTNTYTRVLEFKC 255  
 QY 243 KHKSPKREANPCPHHQCPRRLSSAAPTGGPLTSHQYHNPPIHSSVSGVDPISELRN 302  
 DB 256 KHKSPKREANPCPHHQCPRRLSSAAPTGGPLTSHQYHNPPIHSSVSGVDPISELRN 315  
 QY 303 KGFORGASQELKAVRSSVEEBC 326

DB 316 KGFORGASQELKAVRSSVEEBC 339  
 |||||  
 RESULT 7  
 AAM93907  
 ID AAM93907 standard; protein, 275 AA.  
 XX  
 AC AAM93907;  
 XX  
 DT 06-NOV-2001 (first entry)  
 XX  
 DE Human polypeptide, SEQ ID NO: 4055.  
 XX  
 KM Human; full length cDNA; cDNA synthesis; oligo-capping.  
 XX  
 OS Homo sapiens.  
 XX  
 PN EP1130094-A2.  
 XX  
 PD 05-SEP-2001.  
 XX  
 PF 07-JUL-2000; 2000EP-00114089.  
 XX  
 PR 08-JUL-1999; 99JP-00194486.  
 PR 11-JAN-2000; 2000JP-00118774.  
 PR 02-MAY-2000; 2000JP-00183765.  
 XX  
 PA (HELI-) HELIX RES INST.  
 XX  
 PI Oca T, Nishikawa T, Isegai T, Hayaishi K, Ishii S, Kawai Y,  
 PI Wakamatsu A, Sugiyama T, Nagai K, Kojima S, Otsuki T, Koga H,  
 DR WPI; 2001-524255/58.  
 DR N-PSDB; AAK94869.  
 XX  
 PT 830 Primers useful for synthesizing full length cDNA clones and their use  
 PT in genetic manipulation.  
 XX  
 PS Claim 8; SEQ ID NO 4055; 1380bp + Sequence listing; English.  
 CC The invention relates to primers for synthesizing full length cDNA  
 CC clones. 830 cDNA molecules encoding a human protein have been isolated  
 CC and nucleotide sequences of 5'- and 3'-ends of the cDNA molecules have  
 CC been determined. Primers for synthesizing the full length cDNA are useful  
 CC for clarifying the function of the protein encoded by the cDNA. The full  
 CC length clones were obtained by construction of full length enriched cDNA  
 CC libraries that were synthesised by the oligo-capping method. The primers  
 CC enable the production of the full length cDNA easily without any special  
 CC methods. The present sequence is a polypeptide encoded by a full length  
 CC human cDNA of the invention. Note: The sequence data for this patent did  
 CC not form part of the printed specification, but was obtained in CD-ROM  
 CC format directly from EPO  
 XX  
 SQ Sequence 275 AA;  
 Query Match 83.5%; Score 1450.5; DB 4; Length 275;  
 Best Local Similarity 84.0%; Pred. No. 4.7e-145;  
 Matches 274; Conservative 1; Mismatches 0; Indels 51; Gaps 1;  
 QY 1 MAAMELSKAFSGQRTLLSLNLSLSTSTSLSNYFVGQKPKPLCEKGLAKCPD 60  
 DB 1 MAAMELSKAFSGQRTLLSLNLSLSTSTSLSNYFVGQKPKPLCEKGLAKCPD 60  
 QY 61 MPVSLDGTNTSTQEVVQNMETGDRFGRSFRSGMWSCEETVEEPEGRCSFIELTP 120  
 DB 61 MPVSLDGTNTSTQEVVQNMETGDRFGRSFRSGMWSCEETVEEPEGRCSFIELTP 120  
 QY 121 PAKRELILWLSLGTQITTYIGLQPLISFLILLTDLTGPNPAGKLSAPAAVSSVLSGLGM 180  
 DB 121 PAKR-----GLGLGM 129  
 QY 181 VAMMYSGVFOATVNLGPEDEMRPHVWNYGMAYMMLSTCCMAASAVTTFTNTYTRVLEF 240

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Db      130 VAHMMYSGVFQATVNLGPEDMRPHVMNGMAFYMAMLSFCCMASAVTTFTNTTRVLLEF 189
QY      241 KCKHKSFPKXENNCPLPHHQCPRLSSAAPTGVLTSTYHQYNQPIHSVSEGVDFYSEL 300
Db      190 KCKHKSFPKXENNCPLPHHQCPRLSSAAPTGVLTSTYHQYNQPIHSVSEGVDFYSEL 249
QY      301 RNKGFORGASOBLKEAVRSSVEEQC 326
Db      250 RNKGFORGASOBLKEAVRSSVEEQC 275

RESULT 8
ADL32022
ID      ADL32022 standard; protein; 275 AA.
AC      ADL32022;
XX
XX      20-MAY-2004 (first entry)
DT
XX      Human protein encoded by a full length cDNA clone SeqID 4055.
XX
XX      human; medicine; signal transduction; glycoprotein; transcription;
XX      oligo-capping method.
XX
XX      Homo sapiens.
XX
XX      EPI396543-A2.
XX
XX      10-MAR-2004.
XX
XX      07-JUL-2000; 2003EP-00025638.
XX
XX      08-JUL-1999; 99JP-00194486.
XX
XX      11-JAN-2000; 2000JP-00118774.
XX
XX      02-MAY-2000; 2000JP-00183865.
XX
XX      07-JUL-2000; 2000EP-00114089.
XX
XX      (REAS-) RES ASSOC BIOTECHNOLOGY.
XX
XX      Oca T, Nishikawa T, Iacgai T, Hayashi K, Ishii S, Kawai Y,
XX      Wakamatsu A, Sugiyama T, Nagai K, Kojima S, Otsubki T, Koga H;
XX
XX      WPI; 2004-204755/20.
XX
XX      N-PSDB; ADL32021.
XX
XX      New oligonucleotide primers (830 cDNAs) useful for synthesizing full
XX      length human cDNAs.
XX
XX      Example 1; SEQ ID NO 4055; 1340bp; English.
XX
XX      This invention relates to a novel primers useful for synthesizing full
XX      length cDNA molecules that encode human proteins. Specifically, it refers
XX      to secretory or membrane proteins that are potential therapeutic agents/
XX      target molecules in the field of medicine, and in particular genes
XX      encoding proteins that are associated with signal transduction,
XX      glycoproteins and transcription. The present invention describes a method
XX      for efficiently cloning a full length human cDNA from both the 5' and 3'
XX      ends using the oligo-capping method. This polypeptide sequence is a full
XX      length human protein of the invention.
XX
XX      Sequence 275 AA;
SQ
Query Match      83.5%; Score 1450.5; DB 8; Length 275;
Best Local Similarity 84.0%; Pred. No. 4,7e-145;
Matches 274; Conservative 1; Mismatches 0; Indels 51; Gaps 1;

QY      1 MAHMBLSKAFSGGORTLSAITSLSLSPFTSLSNVYMGVQKVPKLCCKLAKCFD 60
Db      1 MAHMBLSKAFSGGORTLSAITSLSLSPFTSLSNVYMGVQKVPKLCCKLAKCFD 60
QY      61 MPVSLDGDNTNSTQEVVQYNNMETGDDRFSPRSFGMWLSCBETVEPGERCRSFTELTP 120

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Db      61 MPVSLDGDNTNSTQEVVQYNNMETGDDRFSPRSFGMWLSCBETVEPGERCRSFTELTP 120
QY      121 PAKREILMLSLGQTQTYTIGLOPISFLILLTLTDLTGNAACGAKLSAFAVSSVLSGLIGM 180
Db      121 PAKR-----GLIGM 129
QY      181 VAHMMYSGVFQATVNLGPEDMRPHVMNGMAFYMAMLSFCCMASAVTTFTNTTRVLLEF 240
Db      130 VAHMMYSGVFQATVNLGPEDMRPHVMNGMAFYMAMLSFCCMASAVTTFTNTTRVLLEF 189
QY      241 KCKHKSFPKXENNCPLPHHQCPRLSSAAPTGVLTSTYHQYNQPIHSVSEGVDFYSEL 300
Db      190 KCKHKSFPKXENNCPLPHHQCPRLSSAAPTGVLTSTYHQYNQPIHSVSEGVDFYSEL 249
QY      301 RNKGFORGASOBLKEAVRSSVEEQC 326
Db      250 RNKGFORGASOBLKEAVRSSVEEQC 275

RESULT 9
ABJ19723
ID      ABJ19723 standard; protein; 323 AA.
AC      ABJ19723;
XX
XX      03-APR-2003 (first entry)
DT
XX      Human secreted protein amino acid sequence - SEQ ID NO 191.
XX
XX      Human; protein therapy; immediate hypersensitivity diseases;
XX      allergic disorder; asthmatic disorder; gene therapy; secreted protein;
XX      hay fever; allergic conjunctivitis; allergic rhinitis;
XX      binding partner identification; chromosome identification;
XX      radiation hybrid mapping; long-range restriction mapping.
XX
XX      Homo sapiens.
XX
XX      WO200271188-A2.
XX
XX      03-OCT-2002.
XX
XX      26-MAR-2002; 2002WO-US009239.
XX
XX      27-MAR-2001; 2001US-0278650P.
XX
XX      12-SEP-2001; 2001US-00950082.
XX
XX      12-SEP-2001; 2001US-00950083.
XX
XX      (HDMA-) HUMAN GENOME SCI INC.
XX
XX      Rosen CA, Ruben SM;
XX
XX      WPI; 2003-175010/17.
XX
XX      Use of human secreted proteins and nucleic acids for preparing a
XX      diagnostic or pharmaceutical composition for diagnosing or treating
XX      allergic or asthmatic disorders, e.g. asthma, hay fever, or allergic
XX      conjunctivitis or rhinitis.
XX
XX      Claim 1; Page 644-645; 823bp; English.
XX
XX      The invention comprises the amino acid and coding sequences of human
XX      secreted proteins. The DNA and protein sequences of the invention are
XX      useful for the diagnosis and treatment of allergic disorders, asthmatic
XX      disorders and immediate hypersensitivity diseases (e.g. hay fever,
XX      allergic conjunctivitis and allergic rhinitis). The proteins of the
XX      invention are also useful for identifying a binding partner. The nucleic
XX      acids of the invention are also useful for chromosome identification,
XX      radiation hybrid mapping or long-range restriction mapping. The present
XX      amino acid sequence represents a human secreted protein of the invention
XX
XX      Sequence 323 AA;
SQ
Query Match      70.9%; Score 1232; DB 6; Length 323;

```

Best Local Similarity 73.0%; Pred. No. 9.8e-122;  
Matches 251; Conservative 10; Mismatches 41; Indels 42; Gaps 6;

QY 4 MELSKAFSGQRTLLSAILSLMSLSFSTTSLSNVFWGTQVPRPLCEKGLAACGPMV 63  
DB 1 MELSKAFSGQRTLLSAILSLMSLSFSTTSLSNVFWGTQVPRPLCEKGLAACGPMV 60  
QY 64 SLGDNTNSTOEVVQVNWETGDDRFSPFRSGMWLSCEETVEBGRCSFIETLTPAK 123  
DB 61 SLGDNTNSTOEVVQVNWETGDDRFSPFRSGMWLSCEETVEBGRCSFIETLTPAK 120  
QY 124 RELIWLSTGQTYIGLQFISFLLLTDLLTGNPACGLKLSAPAAVSSVLSGL----- 178  
DB 121 RKNPMVTPG-NADHLRTSIHQLEPATNRLATHEPCC-----LMAQTERLCCCFPLCVRS 174  
QY 179 -GNVAHMYTQVQVQATVNLGPEDMRPHVWNYGAFY-----AMLSFT-----CC 222  
DB 175 PGDVAAHMYTQVQVQATVNLGPEDMRPHVWNYGAFYMACSPXAAARLSPXSTXTPGWC 234  
QY 223 MASAVTTFTNTYTMVLEFCKHSPKFNPNCLPHHOCPPRLSSAAPVGLTSYHOY 282  
DB 235 WSSSASIV-----KSPKPNPCLPHHOCPPRLSSAAPVGLTSYHOY 279  
QY 283 HNOPIHVSSEGVDFYSELRNKGFORGASQELKEAVSSVEBQC 326  
DB 280 HNOPIHVSSEGVDFYSELRNKGFORGASQELKEAVSSVEBQC 323

## RESULT 10

ABP9774  
ID ABP9774 standard; protein; 323 AA.

XX AC ABP9774;

XX DT 26-MAR-2003 (first entry)

XX DE Human secreted protein SEQ ID NO 718.

XX XX  
KW Human; secreted protein; nocotropic; neuroprotective; cytosolic;  
KW Vitruidae; dermatological; immunosuppressive; anti-inflammatory; anti-HIV;  
KW vulnary; antibacterial; antiparkinsonian; antickling; antianemic;  
KW antiarthritic; cancer; antineumatic; hepatotropic; cerebroprotective;  
KW antiinflammatory; antiallergic; antidiabetic; antidiuretic; anticonvulsant;  
KW antifungal; antiparasitic; cardiac; immune disorder; infection; vaccine;  
KW cardiovascular disorder; neurological disease; nephrotropic;  
KW gene therapy.

XX XX Homo sapiens.

XX XX PN MO200277186-A2.

XX PD 03-OCT-2002.

XX PF 26-MAR-2002; 2002WO-US009188.

XX PR 27-MAR-2001; 2001US-0278650P.

XX PR 12-SEP-2001; 2001US-00950082.

XX PR 12-SEP-2001; 2001US-00950083.

XX PA (HUMA-) HUMAN GENOME SCI INC.

XX PI Rosen CA, Ruben SM;

XX DR WPI, 2003-040583/03.

XX DR N-PSDB; ABZ67195.

XX PT New human secreted proteins encoded by genes contained in cDNA clones  
XX PT (e.g. HGCAC19), useful for preventing, treating or diagnosing e.g. AIDS,  
XX PT multiple sclerosis, herpes virus, leukemia, tick-borne encephalitis or  
XX PT West Nile fever.

XX PS Claim 1; Page 1479; 2423pp; English.

CC The invention relates to novel human genes (ABZ66891-ABZ68209) and the  
CC encoded secreted proteins (ABP99470-ABP99872) useful for preventing,  
CC treating or ameliorating medical conditions e.g. by protein or gene  
CC therapy. The genes are isolated from a range of human tissues disclosed  
CC in the specification. The nucleic acids, protein, antibodies and  
CC (ant)agonists are useful in the diagnosis, treatment and prevention of:  
CC (a) cancer, e.g. breast and ovarian cancer and other cancers of the  
CC adrenal gland, bone, bone marrow, breast, gastrointestinal tract, liver,  
CC lung or urogenital; (b) immune disorders e.g. Addison's disease,  
CC allergies, autoimmune haemolytic anaemia, autoimmune thyroiditis,  
CC diabetes mellitus, Crohn's disease, multiple sclerosis, rheumatoid  
CC arthritis and ulcerative colitis; (c) cardiovascular disorders such as  
CC myocardial ischaemia; (d) wound healing; (e) neurological diseases e.g.  
CC cerebral anoxia and epilepsy; and (f) infectious diseases such as viral,  
CC bacterial, fungal and parasitic infections

XX SQ Sequence 323 AA;

Query Match 70.9%; Score 1232; DB 6; Length 323;

Best Local Similarity 73.0%; Pred. No. 9.8e-122; Indels 42; Gaps 6;

Matches 251; Conservative 10; Mismatches 41; Indels 42; Gaps 6;

QY 4 MELSKAFSGQRTLLSAILSLMSLSFSTTSLSNVFWGTQVPRPLCEKGLAACGPMV 63  
DB 1 MELSKAFSGQRTLLSAILSLMSLSFSTTSLSNVFWGTQVPRPLCEKGLAACGPMV 60  
QY 64 SLGDNTNSTOEVVQVNWETGDDRFSPFRSGMWLSCEETVEBGRCSFIETLTPAK 123  
DB 61 SLGDNTNSTOEVVQVNWETGDDRFSPFRSGMWLSCEETVEBGRCSFIETLTPAK 120  
QY 124 RELIWLSTGQTYIGLQFISFLLLTDLLTGNPACGLKLSAPAAVSSVLSGL----- 178  
DB 121 RKNPMVTPG-NADHLRTSIHQLEPATNRLATHEPCC-----LMAQTERLCCCFPLCVRS 174  
QY 179 -GNVAHMYTQVQVQATVNLGPEDMRPHVWNYGAFY-----AMLSFT-----CC 222  
DB 175 PGDVAAHMYTQVQVQATVNLGPEDMRPHVWNYGAFYMACSPXAAARLSPXSTXTPGWC 234  
QY 223 MASAVTTFTNTYTMVLEFCKHSPKFNPNCLPHHOCPPRLSSAAPVGLTSYHOY 282  
DB 235 WSSSASIV-----KSPKPNPCLPHHOCPPRLSSAAPVGLTSYHOY 279  
QY 283 HNOPIHVSSEGVDFYSELRNKGFORGASQELKEAVSSVEBQC 326  
DB 280 HNOPIHVSSEGVDFYSELRNKGFORGASQELKEAVSSVEBQC 323

## RESULT 11

ABR01267  
ID ABR01267 standard; protein; 323 AA.

XX AC ABR01267;

XX DT 12-MAY-2003 (first entry)

XX DE Human gene 321-encoded secreted protein HTEB69, SEQ ID NO:748.

XX XX  
KW Human; secreted protein; cancer; tumour; hyperproliferative disorder;  
KW autoimmune disorder; inflammation; angiotensin diseases; AIDS;  
KW acquired immunodeficiency syndrome; hepatitis; anaemia; wound healing;  
KW drug screening; chromosome identification; chromosome mapping;  
KW cytotoxic; gene therapy; antiinflammatory; immunomodulator; anti-HIV;  
KW antianemic; vulnary.

XX XX Homo sapiens.

XX PN MO200277013-A2.

XX PD 03-OCT-2002.

XX PF 26-MAR-2002; 2002WO-US009370.

XX PR 27-MAR-2001; 2001US-0278650P.



PR 12-SEP-2001; 2001US-00950082.  
 PR 12-SEP-2001; 2001US-00950083.  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 PI Rosen CA, Ruben SM;  
 DR WPI; 2003-040578/03.  
 DR N-PSDB; AB273601.  
 PT New human secreted proteins and nucleic acids, useful for detecting or  
 PT treating cancer or other hyperproliferative disorders, autoimmune  
 PT disorders, inflammatory disorders, HIV disease, hepatitis or anemia.  
 XX  
 XX Claim 13; Page 1479; 2474bp; English.  
 XX  
 XX AB273281-AB273697 represent cDNAs corresponding to 391 human secreted  
 CC protein genes, and ABP00947-ABP01363 represent the proteins they encode.  
 CC AB273698-AB274687 represent human secreted protein genomic fragments. The  
 CC invention also encompasses antibodies specific for the secreted proteins,  
 CC the use of the secreted proteins in drug screening and recombinant  
 CC vectors and host cells comprising a nucleic acid of the invention. The  
 CC secreted proteins are thought to be involved in biological activities  
 CC associated with cellular signalling, cellular differentiation, cell  
 CC migration, prohormone activation and neurotransmitter activity. The  
 CC secreted proteins, nucleic acids encoding them, antibodies or antibody  
 CC fragments specific for the secreted proteins, and modulators of protein  
 CC activity are useful for diagnosing or treating cancers or other  
 CC hyperproliferative disorders. Additionally, the secreted proteins and  
 CC their nucleic acids may also be used in the treatment of autoimmune  
 CC disorders, inflammatory disorders, diseases involving angiogenesis, AIDS  
 CC (acquired immunodeficiency syndrome), hepatitis, anemia, and to promote  
 CC wound healing. Nucleic acids of the invention may be used for chromosome  
 CC identification, chromosome mapping, in gene therapy, for identifying  
 CC individuals from minute biological samples, as hybridisation probes, and  
 CC as molecular weight markers. The present sequence represents a human  
 CC secreted protein of the invention  
 XX  
 XX Sequence 323 AA:  
 XX  
 Query Match 70.9%; Score 1232; DB 6; Length 323;  
 Best Local Similarity 73.0%; Pred. No. 9.8e-122;  
 Matches 251; Conservative 10; Mismatches 41; Indels 42; Gaps 6;  
 QY 4 MELSKAFSGQRTLLSAILSMLSLSFSTTSLSNVYFVGQKPKLCEKGLAAKCFDMPV 63  
 DB 1 MELSKAFSGQRTLLSAILSMLSLSFSTTSLSNVYFVGQKPKLCEKGLAAKCFDMPV 60  
 QY 64 SLDDGNTNSTQGVVQYNNMETGDDRFSPFRSGMWLSCEETVEEGERCRSFIELTPPAK 123  
 DB 61 SLDDGNTNSTQGVVQYNNMETGDDRFSPFRSGMWLSCEETVEEGERCRSFIELTPPAK 120  
 QY 124 REILWLSLGTQITTYIGLQFISFLLLTDLTLTGNPACGLKLSAFAVSVLSGLT----- 178  
 DB 121 RENPWYIPIG-NADHLARTSIHQLPATNRLATMHEPC-----LMAQTERLCCCFPCPVRS 174  
 QY 179 -GNVAHMYTSQVFOATVNLGPEPDMRPYVWNYGMAFYM-----AWLSFT-----CC 222  
 DB 175 PGDVAAHMYTSQVFOATVNLGPEPDMRPYVWNYGMAFYMAQSPSYAAMRRRLSPXSTYTPGWC 234  
 QY 223 MASAVTTPTNYTYMVLFEFKSKSPKPNPNCPLPHHOCPPRLTSAAPTGVGLTYSYHQY 282  
 DB 235 WSSSAATV-----KSRKENPNCPLPHHOCPPRLTSAAPTGVGLTYSYHQY 279  
 QY 283 HNPPIHSVSEGVDFYSELNKGFORGASQELKEAVSVSEBQC 326  
 DB 280 HNPPIHSVSEGVDFYSELNKGFORGASQELKEAVSVSEBQC 323  
 RESULT 12  
 ADA98352  
 ID ADA98352 standard; protein; 323 AA.  
 XX

AC ADA98352;  
 XX  
 DT 20-NOV-2003 (first entry)  
 XX  
 DE Human secreted protein sequence #193.  
 XX  
 KW human; secreted protein; cardiovascular disorder; arrhythmia;  
 KW atherosclerosis; stroke; endocarditis; congestive heart failure;  
 KW rheumatic heart disease; cardiomyopathy; haemorrhoids; varicose veins;  
 KW migraine; thrombosis; neural disorder; immune system disorder;  
 KW muscular disorder; reproductive disorder; gastrointestinal disorder;  
 KW pulmonary disorder; renal disorder; proliferative disorder; cancer.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO2003004623-A2.  
 XX  
 PD 16-JAN-2003.  
 XX  
 XX 26-MAR-2002; 2002WO-US009922.  
 PF  
 XX 27-MAR-2001; 2001US-0278650P.  
 PR 12-SEP-2001; 2001US-00950082.  
 PR 12-SEP-2001; 2001US-00950083.  
 XX  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 PI Rosen CA, Ruben SM;  
 DR WPI; 2003-247946/24.  
 XX  
 PT New human secreted polypeptide and nucleic acid molecules, useful for  
 PT diagnosing, preventing, prognosticating or treating cardiovascular  
 PT disorders (e.g. arrhythmia, atherosclerosis, cardiomyopathy, or  
 PT thrombosis).  
 XX  
 XX Claim 1; SEQ ID NO 460; 1572bp; English.  
 XX  
 CC The invention comprises the amino acid and coding sequence of human  
 CC secreted proteins. The DNA and protein sequences of the invention are  
 CC useful in the treatment of cardiovascular disorders, such as: arrhythmia,  
 CC atherosclerosis, stroke, endocarditis, congestive heart failure,  
 CC rheumatic heart disease, cardiomyopathy, haemorrhoids, varicose veins,  
 CC migraine, or thrombosis. The DNA and protein sequences may also be used  
 CC for treating or preventing: neural disorders, immune system disorders,  
 CC muscular disorders, reproductive disorders, gastrointestinal disorders,  
 CC pulmonary disorders, renal disorders, proliferative disorders and/or  
 CC cancerous diseases. The present amino acid sequence represents a human  
 CC secreted protein of the invention. NOTE: The present sequence is shown on  
 CC the WIPD website.  
 XX  
 XX Sequence 323 AA:  
 XX  
 Query Match 70.9%; Score 1232; DB 6; Length 323;  
 Best Local Similarity 73.0%; Pred. No. 9.8e-122;  
 Matches 251; Conservative 10; Mismatches 41; Indels 42; Gaps 6;  
 QY 4 MELSKAFSGQRTLLSAILSMLSLSFSTTSLSNVYFVGQKPKLCEKGLAAKCFDMPV 63  
 DB 1 MELSKAFSGQRTLLSAILSMLSLSFSTTSLSNVYFVGQKPKLCEKGLAAKCFDMPV 60  
 QY 64 SLDDGNTNSTQGVVQYNNMETGDDRFSPFRSGMWLSCEETVEEGERCRSFIELTPPAK 123  
 DB 61 SLDDGNTNSTQGVVQYNNMETGDDRFSPFRSGMWLSCEETVEEGERCRSFIELTPPAK 120  
 QY 124 REILWLSLGTQITTYIGLQFISFLLLTDLTLTGNPACGLKLSAFAVSVLSGLT----- 178  
 DB 121 RENPWYIPIG-NADHLARTSIHQLPATNRLATMHEPC-----LMAQTERLCCCFPCPVRS 174  
 QY 179 -GNVAHMYTSQVFOATVNLGPEPDMRPYVWNYGMAFYM-----AWLSFT-----CC 222  
 DB 175 PGDVAAHMYTSQVFOATVNLGPEPDMRPYVWNYGMAFYMAQSPSYAAMRRRLSPXSTYTPGWC 234





PS Claim 11; SEQ ID NO 2183; 2081bp + Sequence Listing; English.

XX CC The invention relates to novel genes (AB094499-AB090855) and proteins  
 CC (AB094040-AB090444) useful for preventing, treating or ameliorating  
 CC medical conditions e.g. by protein or gene therapy. The genes are  
 CC isolated from a range of human tissues disclosed in the specification.  
 CC The nucleic acids, proteins, antibodies and (ant)agonists are useful in  
 CC the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and  
 CC ovarian cancer and other cancers of the adrenal gland, bone, bone marrow,  
 CC breast, gastrointestinal tract, liver, lung, or urogenital; (b) immune  
 CC disorders e.g. Addison's disease, allergies, autoimmune haemolytic  
 CC anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's disease,  
 CC multiple sclerosis, rheumatoid arthritis and ulcerative colitis; (c)  
 CC cardiovascular disorders such as myocardial ischaemia; (d) wound healing  
 CC ; (e) neurological diseases such as cerebral anoxia and epilepsy; and (f)  
 CC infectious diseases such as viral, bacterial, fungal and parasitic  
 CC infections. Note: The sequence data for this patent did not form part of  
 CC the printed specification, but was obtained in electronic format directly  
 CC from WIPO at ftp.wipo.int/pub/published\_pct\_sequences

XX SQ Sequence 330 AA;

Query Match 62.5%; Score 1086; DB 5; Length 330;  
 Best Local Similarity 98.5%; Pred. No. 3.3e-106;  
 Matches 201; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 123 KREILMLSGTQITTYIGLPISFLILLTLGNPACGLKLSAFPAVSSVSLGLGWA 182  
 DB 127 KREILMLSGTQITTYIGLPISFLILLTLGNPACGLKLSAFPAVSSVSLGLGWA 186

QY 183 HMYNSQVPAATVNLGPEDRPHVMYNGAFYMAWLSFTCCMASAVTTFTYTRMVLFFKC 242  
 DB 187 HMYNSQVPAATVNLGPEDRPHVMYNGAFYMAWLSFTCCMASAVTTFTYTRMVLFFKC 246

QY 243 KSKSKFKNPNCIPHHQCFPRRLSSAAPTGVGLTSYHQNOPHISVSEGVDFSELN 302  
 DB 247 KSKSKFKNPNCIPHHQCFPRRLSSAAPTGVGLTSYHQNOPHISVSEGVDFSELN 306

QY 303 KGFORGASQELKEAVRSSVEECC 326  
 DB 307 KGFORGASQELKEAVRSSVEECC 330

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 AAM93674  
 ID AAM93674 standard; protein; 343 AA.  
 XX AC AAM93674;  
 XX DT 06-NOV-2001 (first entry)  
 XX DE Human polypeptide, SEQ ID NO: 3562.  
 XX KW Human, full length cDNA; cDNA synthesis; oligo-capping.  
 XX OS Homo sapiens.  
 XX PN EPI130094-A2.  
 XX PD 05-SEP-2001.  
 XX PF 07-JUL-2000; 2000BP-00114089.  
 XX PR 08-JUL-1999; 993P-00194486.  
 XX PR 11-JAN-2000; 2000JP-00118774.  
 XX PR 02-MAY-2000; 2000JP-00183765.  
 XX PA (HELI-) HELIX RES INST.  
 XX PI Ota T, Nishikawa T, Isegai T, Hayaishi K, Ishii S, Kawai Y,  
 XX PI Wakamatsu A, Sugiyama T, Nagai K, Kojima S, Otsuki T, Koga H,  
 XX DR WPI; 2001-524255/58.

DR N-PsDB; AAK94609.

XX PT 830 Primers useful for synthesizing full length cDNA clones and their use  
 XX in genetic manipulation.

XX CC Claim 8; SEQ ID NO 3562; 1380bp + Sequence Listing; English.

XX CC The invention relates to primers for synthesizing full length cDNA  
 CC clones. 830 cDNA molecules encoding a human protein have been isolated  
 CC and nucleotide sequences of 5'- and 3'-ends of the cDNA molecules have  
 CC been determined. Primers for synthesizing the full length cDNA are useful  
 CC for clarifying the function of the protein encoded by the cDNA. The full  
 CC length clones were obtained by construction of full length enriched cDNA  
 CC libraries that were synthesised by the oligo-capping method. The primers  
 CC enable the production of the full length cDNA easily without any special  
 CC methods. The present sequence is a polypeptide encoded by a full length  
 CC human cDNA of the invention. Note: The sequence data for this patent did  
 CC not form part of the printed specification, but was obtained in CD-ROM  
 CC format directly from EPO

XX SQ Sequence 343 AA;

Query Match 56.8%; Score 987.5; DB 4; Length 343;  
 Best Local Similarity 61.9%; Pred. No. 1e-95;  
 Matches 226; Conservative 13; Mismatches 65; Indels 61; Gaps 13;

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 DB 1 MAKWELSKAFSGGORTLLSAILSMLSSTSTLSNWFVGTOVKPKLCEKGLAAKCPD 60

QY 61 MPVSLDGDNTSTOEVQYNNMETGDDRFPSFGMWLSCETVEBBERCRSFIELTP 120  
 DB 61 MPVSLDGDNTSTOEVQYNNMETGDDRFPSFGMWLSCETVEBBERCRSFIELTP 120

QY 121 PAKREILMLSGTQITTYIGLPISFLILLTLGNPACGLKLSAFPAVSSVSLGLG 179  
 DB 121 PAKREILMLSGTQITTYIGLPISFLILLTLGNPACGLKLSAFPAVSSVSLGLG 166

QY 180 --MVA-----HMYNSQVPA--ATTNLGPEDRPHVMYNGAFYMAWLSFTCCMASAVTT 229  
 DB 167 NPMVLPGNADHLAKRSTYQLPPATRLATH--WEPCLM-----AQTRLLCCCFPCVRS 218

QY 230 -----FNTYTRMV-----LEFKC-----KSKSK--FKENPNC--LPH--HHQC 261  
 DB 219 PGDGGPHVFTSLPBDCCOLGSRULETTLGLMLGLHGLALHLHGVGCHNLGHVHHQC 278

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 DB 279 FPRRLSSAAPTGVGLTSYHQNOPHISVSEGVDFSELNKKGFORGASQELKEAVRSSV 338

QY 322 EEECC 326  
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Search completed: July 14, 2005, 20:27:27  
 Job time : 111.417 secs

GenCore version 5.1.6  
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OM protein - protein search, using bw model

Run on: July 14, 2005, 20:16:41 ; Search time 98.9192 Seconds  
(without alignments)  
1273.204 Million cell updates/sec

Title: US-10-019-151C-3

Perfect score: 1738  
Sequence: 1 MAKMBLSKAPSGGRTLLSAI.....RGASQELKAVRSVREEQ 326

Scoring table:

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Gapop 10.0 , Gapext 0.5

Searched: 1726220 seqs, 386332138 residues

Total number of hits satisfying chosen parameters: 1726220

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications AA:  
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysts of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1725	99.3	339	US-09-729-674-138	Sequence 138, App
2	1725	99.3	339	US-10-913-553-138	Sequence 138, App
3	1086	62.5	330	US-10-264-237-2183	Sequence 2183, App
4	657.5	37.8	285	US-09-989-722-272	Sequence 272, App
5	657.5	37.8	285	US-09-989-723-272	Sequence 272, App
6	657.5	37.8	285	US-09-989-729-272	Sequence 272, App
7	657.5	37.8	285	US-09-989-727-272	Sequence 272, App
8	657.5	37.8	285	US-09-989-731-272	Sequence 272, App
9	657.5	37.8	285	US-09-989-732-272	Sequence 272, App
10	657.5	37.8	285	US-09-991-073-272	Sequence 272, App
11	657.5	37.8	285	US-09-990-442-272	Sequence 272, App

12	657.5	37.8	285	US-09-991-163-272	Sequence 272, App
13	657.5	37.8	285	US-09-993-604-272	Sequence 272, App
14	657.5	37.8	285	US-09-990-456-272	Sequence 272, App
15	657.5	37.8	285	US-09-989-721-272	Sequence 272, App
16	657.5	37.8	285	US-09-992-598-272	Sequence 272, App
17	657.5	37.8	285	US-09-989-293A-272	Sequence 272, App
18	657.5	37.8	285	US-09-989-735-272	Sequence 272, App
19	657.5	37.8	285	US-09-990-444-272	Sequence 272, App
20	657.5	37.8	285	US-09-991-181-272	Sequence 272, App
21	657.5	37.8	285	US-09-989-730-272	Sequence 272, App
22	657.5	37.8	285	US-09-990-436-272	Sequence 272, App
23	657.5	37.8	285	US-09-993-687-272	Sequence 272, App
24	657.5	37.8	285	US-09-989-734-272	Sequence 272, App
25	657.5	37.8	285	US-09-997-653-272	Sequence 272, App
26	657.5	37.8	285	US-09-989-724-272	Sequence 272, App
27	657.5	37.8	285	US-09-989-728-272	Sequence 272, App
28	657.5	37.8	285	US-09-990-441-272	Sequence 272, App
29	657.5	37.8	285	US-09-993-667-272	Sequence 272, App
30	657.5	37.8	285	US-09-997-428-272	Sequence 272, App
31	657.5	37.8	285	US-09-997-666-272	Sequence 272, App
32	657.5	37.8	285	US-09-990-438-272	Sequence 272, App
33	657.5	37.8	285	US-09-990-562-272	Sequence 272, App
34	657.5	37.8	285	US-09-990-711-272	Sequence 272, App
35	657.5	37.8	285	US-09-989-726-272	Sequence 272, App
36	657.5	37.8	285	US-09-998-156-272	Sequence 272, App
37	657.5	37.8	285	US-09-990-437-272	Sequence 272, App
38	657.5	37.8	285	US-09-991-157-272	Sequence 272, App
39	657.5	37.8	285	US-09-997-514-272	Sequence 272, App
40	657.5	37.8	285	US-09-997-573-272	Sequence 272, App
41	657.5	37.8	285	US-09-991-172-272	Sequence 272, App
42	657.5	37.8	285	US-09-990-726-272	Sequence 272, App
43	657.5	37.8	285	US-09-997-555-272	Sequence 272, App
44	657.5	37.8	285	US-09-997-601-272	Sequence 272, App
45	657.5	37.8	285	US-09-990-443-272	Sequence 272, App

#### ALIGNMENTS

RESULT 1  
US-09-729-674-138  
Sequence 138, Application US/09729674  
Patent No. US20010039335A1  
GENERAL INFORMATION:  
APPLICANT: Jacobs, Kenneth  
APPLICANT: McCoy, John M.  
APPLICANT: LaVallie, Edward R.  
APPLICANT: Collins-Racie, Lisa A.  
APPLICANT: Byrne, Cheryl  
APPLICANT: Merberg, David  
APPLICANT: Treacy, Maurice  
APPLICANT: Agostino, Michael J.  
APPLICANT: Steindinger II, Robert J.  
APPLICANT: Spaulding, Vikki  
APPLICANT: Wong, Gordon G.  
APPLICANT: Clark, Hilary  
APPLICANT: Fechtel, Kim  
TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES ENCODING THEM  
FILE REFERENCE: 6055-64X  
CURRENT APPLICATION NUMBER: US/09/729, 674  
CURRENT FILING DATE: 2000-12-04  
PRIOR APPLICATION NUMBER: 09/539, 330  
PRIOR FILING DATE: 2000-03-30  
NUMBER OF SEQ ID NOS: 283  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 138  
LENGTH: 339  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-729-674-138  
Query Match 99.3%; Score 1725; DB 9; Length 339;

Best Local Similarity 99.7%; Pred. No. 1.6e-173;  
Matches 333; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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QY 3 KHELSTAFSGGORTLSAIIISMLSLSPSTTSLSNVYFVGTVQVKKPLCEKGLAAKCFDMP 62
DB 16 EHELSTAFSGGORTLSAIIISMLSLSPSTTSLSNVYFVGTVQVKKPLCEKGLAAKCFDMP 75
QY 63 VSLDGTNTSTQEVVQYNNMETGDDRFSPFSFRSGMWLSCBEYVEEGECRSFIELTPPA 122
DB 76 VSLDGTNTSTQEVVQYNNMETGDDRFSPFSFRSGMWLSCBEYVEEGECRSFIELTPPA 135
QY 123 KREILWLSIGTOITYIGLOFISFLILLTDLITGNPACGLKLSAFAVSSVLSGLGMVA 182
DB 136 KREILWLSIGTOITYIGLOFISFLILLTDLITGNPACGLKLSAFAVSSVLSGLGMVA 195
QY 183 HMYSQVFOATVNLGPEDMRPHVMNYGMAFYMAWLSFTCCMASAVTTFTNTYTRMVLBFKC 242
DB 196 HMYSQVFOATVNLGPEDMRPHVMNYGMAFYMAWLSFTCCMASAVTTFTNTYTRMVLBFKC 255
QY 243 KHSKSPKENPCLPHHHQCFPRRLSSAAPVGPLTSYHQYNQPHHSVEGVDFYSELRN 302
DB 256 KHSKSPKENPCLPHHHQCFPRRLSSAAPVGPLTSYHQYNQPHHSVEGVDFYSELRN 315
QY 303 KGFORGASOELKEAVRSSVVEEQC 326
DB 316 KGFORGASOELKEAVRSSVVEEQC 339

RESULT 2
US-10-913-553-138
; Sequence 138, Application US/10913553
; Publication No. US20050003491A1
; GENERAL INFORMATION:
; APPLICANT: Uacobe, Kenneth
; APPLICANT: McCoy, John M.
; APPLICANT: Lavalie, Edward R.
; APPLICANT: Collins-Racie, Lisa A.
; APPLICANT: Evans, Cheryl
; APPLICANT: Merberg, David
; APPLICANT: Treacy, Maurice
; APPLICANT: Agoetino, Michael J.
; APPLICANT: Steinhinger II, Robert J.
; APPLICANT: Spaulding, Vikki
; APPLICANT: Mong, Gordon G.
; APPLICANT: Clark, Hilary
; APPLICANT: Fecthel, Kim
; APPLICANT: Genetics Institute, Inc.
; TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES ENCODING THEM
; FILE REFERENCE: 6055-64X
; CURRENT APPLICATION NUMBER: US/10/913,553
; PRIOR APPLICATION NUMBER: US/09/539,330
; PRIOR FILING DATE: 2000-03-30
; NUMBER OF SEQ ID NOS: 283
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 138
; LENGTH: 339
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-913-553-138

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Query Match 99.3%; Score 1725; DB 17; Length 339;  
Best Local Similarity 99.7%; Pred. No. 1.6e-173;  
Matches 333; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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QY 3 KHELSTAFSGGORTLSAIIISMLSLSPSTTSLSNVYFVGTVQVKKPLCEKGLAAKCFDMP 62
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QY 63 VSLDGTNTSTQEVVQYNNMETGDDRFSPFSFRSGMWLSCBEYVEEGECRSFIELTPPA 122
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DB 316 KGFORGASOELKEAVRSSVVEEQC 339

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RESULT 3  
US-10-264-237-2183

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; Sequence 2183, Application US/10264237
; Publication No. US20040009491A1
; GENERAL INFORMATION:
; APPLICANT: Birse et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: P4131p1
; CURRENT APPLICATION NUMBER: US/10/264,237
; PRIOR FILING DATE: 2002-10-04
; PRIOR APPLICATION NUMBER: PCT/US01/16450
; PRIOR FILING DATE: 2001-05-18
; PRIOR APPLICATION NUMBER: US 60/205,515
; NUMBER OF SEQ ID NOS: 2876
; SOFTWARE: PatentIn Ver. 3.1
; SEQ ID NO 2183
; LENGTH: 330
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-264-237-2183

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Query Match 62.5%; Score 1086; DB 15; Length 330;  
Best Local Similarity 98.5%; Pred. No. 6.9e-106;  
Matches 201; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

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QY 183 HMYSQVFOATVNLGPEDMRPHVMNYGMAFYMAWLSFTCCMASAVTTFTNTYTRMVLBFKC 242
DB 187 HMYSQVFOATVNLGPEDMRPHVMNYGMAFYMAWLSFTCCMASAVTTFTNTYTRMVLBFKC 246
QY 243 KHSKSPKENPCLPHHHQCFPRRLSSAAPVGPLTSYHQYNQPHHSVEGVDFYSELRN 302
DB 247 KHSKSPKENPCLPHHHQCFPRRLSSAAPVGPLTSYHQYNQPHHSVEGVDFYSELRN 306
QY 303 KGFORGASOELKEAVRSSVVEEQC 326
DB 307 KGFORGASOELKEAVRSSVVEEQC 330

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RESULT 4

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US-09-989-722-272
; Sequence 272, Application US/09989722
; Patent No. US20020072067A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter

```

APPLICANT: Gertlesen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gurney, Austin L.  
APPLICANT: KJavein, Ivar J.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Metcane, Colin K.  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P2730P1C63  
CURRENT APPLICATION NUMBER: US/09/989,722  
CURRENT FILING DATE: 2001-11-19  
PRIOR APPLICATION NUMBER: 60/049787  
PRIOR FILING DATE: 1997-06-16  
PRIOR APPLICATION NUMBER: 60/062250  
PRIOR FILING DATE: 1997-10-17  
PRIOR APPLICATION NUMBER: 60/065186  
PRIOR FILING DATE: 1997-11-12  
PRIOR APPLICATION NUMBER: 60/065311  
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PRIOR FILING DATE: 1998-03-20  
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PRIOR FILING DATE: 1998-05-07  
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PRIOR FILING DATE: 1998-06-05

PRIOR APPLICATION NUMBER: 60/088655  
PRIOR FILING DATE: 1998-06-09  
PRIOR APPLICATION NUMBER: 60/088734  
PRIOR FILING DATE: 1998-06-10  
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PRIOR FILING DATE: 1998-06-22  
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PRIOR FILING DATE: 1998-06-22  
PRIOR APPLICATION NUMBER: 60/090254  
PRIOR FILING DATE: 1998-06-22  
PRIOR APPLICATION NUMBER: 60/090349  
PRIOR FILING DATE: 1998-06-23  
PRIOR APPLICATION NUMBER: 60/090355  
PRIOR FILING DATE: 1998-06-23  
PRIOR APPLICATION NUMBER: 60/090429  
PRIOR FILING DATE: 1998-06-24  
PRIOR APPLICATION NUMBER: 60/090431  
PRIOR FILING DATE: 1998-06-24  
PRIOR APPLICATION NUMBER: 60/090435  
PRIOR FILING DATE: 1998-06-24  
PRIOR APPLICATION NUMBER: 60/090444  
PRIOR FILING DATE: 1998-06-24  
PRIOR APPLICATION NUMBER: 60/090445  
PRIOR FILING DATE: 1998-06-24  
PRIOR APPLICATION NUMBER: 60/090472

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; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090535
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090540
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; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/091982
; PRIOR FILING DATE: 1998-07-07
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; PRIOR FILING DATE: 1998-07-09

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Query Match      37.8%; Score 657.5; DB 9; Length 285;
Best Local Similarity 51.6%; Pred. No. 1.3e-60;
Matches 165; Conservative 14; Mismatches 76; Indels 65; Gaps 11;

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DB      1 MAMMELSKAFSGQRTLLSALISMLSLSPFTTSLISNYWVGTVQKVPKCEKGLAAKCPD 60
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DB      121 PAKRGEKGL-----LEPFTLQGPCHPITLPG-----GKRLMEKASLPSPLIGLCKG 166
QY      180 --MVA-----HMWYGVFQ---ATVNLGPEDMRPHVWNYGMAYMWLSFTCCMASAVTT 229
DB      167 NPVAVIGNADHLARTSIHQLPATNRLATH-WEPCLW-----AQTERLCCC----- 211
QY      230 FNTYTMVLEFKCKSKSKSPKKNPN---CLPHHQCPRRLSAA-----PTVGPLTSYH 280
DB      212 -----FLCPVNSPDCGPHDVFTSLPSDCQSLSRLEFTYCELMGLHGLALH 261
QY      281 Q-----YHNPRIHSVSEGV 294
DB      262 LHHGVGCHHLDQVHODGAV 281

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RESULT 5
US-09-989-723-272
; Sequence 272, Application US/09989723
; Patent No. US20020072092A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnovers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gertlisen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Guiney, Austin L.
; APPLICANT: Kljavin, Ivar J.
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; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2730PLC62
; CURRENT APPLICATION NUMBER: US/09/989,723
; PRIOR FILING DATE: 2001-11-19
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;; PRIOR FILING DATE: 1998-07-09

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1 PRIOR APPLICATION NUMBER: 60/092182  
1 PRIOR FILING DATE: 1998-07-09

Query Match 37.8%; Score 657.5; DB 9; Length 285;  
Best Local Similarity 51.6%; Pred. No. 1,3e-60;  
Matches 165; Conservative 14; Mismatches 76; Indels 65; Gaps 11;

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Db 1 MARKELSKAFSGQRTLLSAILSMLSLSPSTTSLSNTPYGTQVNPRLCEKGIACCPD 60  
Qy 61 MPVSLDDDTSTQEVQVQWMEGDDRFSPRSPGKMLSCETVVEPGRCRSFIILTP 120  
Db 61 MPVSLDDDTSTQEVQVQWMEGDDRFSPRSPGKMLSCETVVEPGRCRSFIILTP 120  
Qy 121 PAKREILMISLGTQITVIGLQFISFLLLTDLITGNPACGLKLSAPAAVSVLSGLG- 179  
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Db 212 -----FLCPVNSPFGCGPHDVTSLPSDCQLGSRRLBETTCLEMLGILHGLLH 261  
Qy 281 Q-----YHNPISVSEGV 294  
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RESULT 7  
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Sequence 272, Application US/09989727  
Patent No. US20020072497A1  
GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi J.  
APPLICANT: Baker, Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Batton, Dan L.  
APPLICANT: Ferrara, Napoleone  
APPLICANT: Fong, Sherman  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Geriltsen, Mary B.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gutney, Austin L.  
APPLICANT: Kijavain, Ivar J.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas P.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumaas, Daniel  
APPLICANT: Watanabe, Colin K.  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P2730PLC65  
CURRENT APPLICATION NUMBER: US/09/989,727  
CURRENT FILING DATE: 2001-11-19  
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58	PRIOR APPLICATION NUMBER: 60/088876	58	PRIOR FILING DATE: 1998-06-25
59	PRIOR FILING DATE: 1998-06-11	59	PRIOR APPLICATION NUMBER: 60/090696
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62	PRIOR APPLICATION NUMBER: 60/089440	62	PRIOR FILING DATE: 1998-06-26
63	PRIOR FILING DATE: 1998-06-16	63	PRIOR APPLICATION NUMBER: 60/090863
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67	PRIOR FILING DATE: 1998-06-16	67	PRIOR APPLICATION NUMBER: 60/091478
68	PRIOR APPLICATION NUMBER: 60/089532	68	PRIOR FILING DATE: 1998-07-02
69	PRIOR FILING DATE: 1998-06-17		

PRIOR FILING DATE: 1998-07-02  
PRIOR APPLICATION NUMBER: 60/091633  
PRIOR FILING DATE: 1998-07-02  
PRIOR APPLICATION NUMBER: 60/091978  
PRIOR FILING DATE: 1998-07-07  
PRIOR APPLICATION NUMBER: 60/091982  
PRIOR FILING DATE: 1998-07-07  
PRIOR APPLICATION NUMBER: 60/092182  
PRIOR FILING DATE: 1998-07-09

Query Match 37.8%; Score 657.5; DB 9; Length 285;  
Best Local Similarity 51.6%; Pred. No. 1.3e-60;  
Matches 165; Conservative 14; Mismatches 76; Indels 65; Gaps 11;

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DB 1 MARKELSKAPSGGCTLLSALISMSLSGTTSLSNVFWCTGYKPPPLCKGLAACFD 60  
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DB 121 PAKKGEKGL-----LEFATLQGPCHPTLRF-----GKRLMEKASLSPSLGCGK 166  
QY 180 --WVA-----HMATSOVFQ--ATVNTGPEWRPHVWNYGAFYMANLSFTCCMASAVTT 229  
DB 167 NPVYIPGNADHLHRTSHOLEPPATNRLATH-WBPCLW-----ACTERLCCC----- 211  
QY 230 FNTYTRVNLBPKCKHSGHSFKENRP-----CLPHHQCPRLSSAA-----PTVGPILSYH 280  
DB 212 -----FLCPVRSPPGCGRPDVTSLSPSCQLSRLETTCLEMLGLHGLLH 261  
QY 281 Q-----YHNPRIHSEGV 294  
DB 262 LKHGVGHLLQHNVHQDQAGV 281

RESULT 8  
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Sequence 272, Application US/09989731  
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GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi J.  
APPLICANT: Baker, Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Desnovers, Luc  
APPLICANT: Eaton, Dan L.  
APPLICANT: Ferrara, Napoleone  
APPLICANT: Fong, Sherman  
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APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James  
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APPLICANT: Roy, Margaret Ann  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tuma, Daniel  
APPLICANT: Watanabe, Colin K.  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P2730P1C70  
CURRENT APPLICATION NUMBER: US/09/989, 731  
CURRENT FILING DATE: 2001-11-20

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PRIOR FILING DATE: 1997-06-16  
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;; PRIOR FILING DATE: 1998-06-26  
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;; PRIOR FILING DATE: 1998-06-26  
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;; PRIOR APPLICATION NUMBER: 60/091978  
;; PRIOR FILING DATE: 1998-07-07  
;; PRIOR APPLICATION NUMBER: 60/091982  
;; PRIOR FILING DATE: 1998-07-07  
;; PRIOR APPLICATION NUMBER: 60/092182  
;; PRIOR FILING DATE: 1998-07-09

Query Match 37.8%; Score 657.5; DB 9; length 285;  
Best local Similarity 51.6%; Pred. No. 1.3e-60;  
Matches 165; Conservative 14; Mismatches 76; Indels 65; Gaps 11;

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DB 61 MPVSLDGDNTSTQEVQVQNMETGDDRFSPFRSGMMVSCSEYEBPDERCRSFTELTP 120  
|||  
QY 121 PAKREILMLSLGTQYITGLQPIISPLLLTDLTLGNPACGJKLSAFNAVSSVLSGLLG- 179  
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DB 121 PAKRGEKGL-----LEFATLQGPCHPLTRFG-----GRLEMKASLSPRPGLGCK 166  
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QY 180 --MVA-----IMMYGQVFO--ATVNLGPEDEMRPHVNYGMAFYMAVLSFTCCMASAYTT 229  
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DB 167 NPMVLPGNADHLHRISIHQLPATYRKLATH-WEPCLM-----AQTERLCCC----- 211  
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QY 230 FATYTRMVLFPCKCKSKSPKENPN-----CLPHHOCFPRRLSSAA-----PTVGPITYSH 280  
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DB 212 -----FLCPVRSPEDGPFHDVFTSLPBDQUGSRRLTCTCLBLMLGLHLGLALH 261  
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QY 281 Q-----YHNPRIHVSSEGV 294  
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; Patent No. US20020123463A1  
; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi J.  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan L.  
; APPLICANT: Ferrara, Napoleone  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gerber, Hanspeter  
; APPLICANT: Gerlitsen, Mary E.  
; APPLICANT: Goddard, Audrey  
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; APPLICANT: Kijavlin, Ivar J.  
; APPLICANT: Napier, Mary A.  
; APPLICANT: Pan, James

APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Watanabe, Colin K.  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
APPLICANT: Zhang, Zhenli  
TITLE OR INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE OR INVENTION: Acids Encoding the Same  
FILE REFERENCE: P2730P1C57  
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CURRENT FILING DATE: 2001-11-09  
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/ PRIOR APPLICATION NUMBER: 60/092182
/ PRIOR FILING DATE: 1998-07-09

Query Match      37.8%; Score 657.5; DB 9; Length 285;
Best Local Similarity 51.6%; Pred. No. 1,3e-60;
Matches 165; Conservative 14; Mismatches 76; Indels 65; Gaps 11;

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DB      61 MVSUJGDNTSTQEVVOUWNGWGDGDFRSFRSGMWTSCERTVEEPEGRCSFTILTP 120
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DB      121 PAKRGKGL-----LEFATLQGRCHPTLRFG---GKRLMEKALPBPRLGLCSCK 166
QY      180 --MVA-----HMYSQVFC--ATVNLGREDWPRHVMYNYGMAFYUAWLSFTCCMASAVTT 229
DB      167 NEMVUPGNADHLRHSIHQLPRTNMLATN-WERPCIM-----AQTRRLCCC----- 211
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QY      281 Q-----YHNPDIHSVSEGV 294
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RESULT 10
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; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
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/ APPLICANT: Desnoyers, Luc
/ APPLICANT: Baton, Dan L.
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/ APPLICANT: Kljavin, Ivar J.
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/ APPLICANT: Wood, William I.
/ APPLICANT: Zhang, Zemin
/ TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
/ FILE REFERENCE: P2730P1C15
/ CURRENT APPLICATION NUMBER: US/09/991,073
/ PRIOR FILING DATE: 2001-11-14
/ PRIOR APPLICATION NUMBER: 60/049787
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 PRIOR FILING DATE: 1998-07-07  
 PRIOR APPLICATION NUMBER: 60/091982  
 PRIOR FILING DATE: 1998-07-07  
 PRIOR APPLICATION NUMBER: 60/092182  
 PRIOR FILING DATE: 1998-07-09

Query Match 37.8%; Score 657.5; DB 9; Length 285;  
 Best Local Similarity 51.6%; Pred. No. 1.3e-60;  
 Matches 165; Conservative 14; Mismatches 76; Indels 65; Gaps 11;

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 61 MPVSLDGDTNTSTQEVVQVWMEGTDRFSFRSGMWLSCEBTEVBERGCRSFIEITP 120  
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 121 PARBELWLSLGTQITVIGLQISPLLLTDLITGNPACGLKLSAPAAVSVLSGLLG 179  
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 167 NPNVITGADHILKRITIHQPPATNRLATH-WBPCIM-----KOTERLCCC----- 211  
 230 FNTYTBWVLEPKCKSKSKSPKFNENP---CLPHHQCFPRRLSSNA-----PTVGPLTSYH 280  
 212 -----FLCPVNSPDGGRHDVFTSLPSDCQGLSRRLETTCTCELMWGLHGLALAH 261

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DB 262 LHHGVCHHGHVHOGAGV 281

RESULT 11  
US-09-990-442-272  
; Sequence 272, Application US/09990442  
; Patent No. US20020132252A1  
; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi J.  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan L.  
; APPLICANT: Ferrara, Napoleone  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gerber, Hanspeter  
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; APPLICANT: Goddard, Audrey  
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; APPLICANT: Kijavlin, Ivar J.  
; APPLICANT: Napier, Mary A.  
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; APPLICANT: Paoni, Nicholas P.  
; APPLICANT: Roy, Margaret Ann  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tuma, Daniel  
; APPLICANT: Watanabe, Colin K.  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William I.  
; APPLICANT: Zhang, Zemin  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; FILE OF INVENTION: Acids Encoding the Same  
; FILE REFERENCE: P2730P1C8  
; CURRENT APPLICATION NUMBER: US/09/990,442  
; PRIOR FILING DATE: 2001-11-14  
; PRIOR APPLICATION NUMBER: 60/049787  
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PRIOR FILING DATE: 1998-07-09

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DB 61 MPVSLDGDNTNTSTQEVVQVYVMTGDDRFSFRSFRSGMWSCEBTEVSPGCRSFTELT 120

QY 121 PAKREILMSLGTQITTYIGLQFISFLLLDLITGNPAGGLKLSAPAAVSVLSGLG- 179  
DB 121 PAKRGEKGL-----LEFATLQCPCHPTLRFG-----GKRLMKRSLSPSPGLGCGK 166  
QY 180 --MVA-----HMWYQVFO--ATVNLPSPDMRPHVNVNGAFYMAWLSFTCCMAAVTT 229  
DB 167 NPVAVIPGNADHLRTSTSHQLPATNRLATH-WBPCLM-----AQTERLCCC----- 211  
QY 230 FNTYTRWVLEPKCKGSKSPKENPN---CLPHHQCFPRRLSSAA-----PYVGPLTSYH 280  
DB 212 -----FLCPVNSPBGDGPBHDVFTSLPSDQQLSGRRLLETTCLEMTGLHGLALLH 261  
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## RESULT 12

US-09-991-163-272  
Sequence 272, Application US/09991163  
Patent No. US20020132253A1  
GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi J.  
APPLICANT: Baker, Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Eaton, Dan L.  
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APPLICANT: Roy, Margaret Ann  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Watanabe, Colin K.  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCES: P2730P1C17  
CURRENT APPLICATION NUMBER: US/09/991,163  
PRIOR FILING DATE: 2001-11-14  
PRIOR APPLICATION NUMBER: 60/049787  
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PRIOR APPLICATION NUMBER: 60/087607



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; PRIOR FILING DATE: 1998-07-09
Query Match      37.8%; Score 657.5; DB 9; Length 285;
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DB 61 MPVSLDDTNTSTQEVVQYNWETGDDRFSPRSFPGMMLSCETVEBPGRCRSPILTTP 120
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QY 121 PAKREILMSLGQITITIGQFISFLLLDLITENPACGLKISAPAAVSVLSGLG- 179
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DB 121 PAKRGEKGL-----LEFATLQGPCHPTLRFG-----GKRLMERKASLPSPLGCGK 166
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QY 180 --WVA-----HMWYSGVFO---ATVNLGPDMDRPHVNNYGMAFYMAWLSPTCCMASAVTT 229
   |||||
DB 167 NPWVIFGNADHLHRTSTHQLPAPATNRLATN-WEPCLM-----AOTERLCCC----- 211
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QY 230 FNTYTRWVLEFCKGHSKSPKBNPN---CLPHHQCFPRRLSNA-----PTVGPILTSYH 280
   |||||
DB 212 -----FLCPVRSRPGSGPHDVFTSLPSDCQLGSRULETTCLELWMLGLHGLALLH 261
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QY 281 Q-----YHNPHTSVSEGV 294
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DB 262 LHHGVGCHLQHVDQAGV 281

RESULT 13
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; Patent No. US20020137075A1
; GENERAL INFORMATION:
; APPLICANT: Asphenazi, Av4 J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Deenoyers, Luc
; APPLICANT: Batton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kijavlin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas P.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumaas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2730P1C25
; CURRENT APPLICATION NUMBER: US/09/993,604
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
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 PRIOR FILING DATE: 1998-07-09

Query Match 37.8%; Score 657.5; DB 9; Length 285;  
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 DB 121 PAKRGEKGL-----LEFATLQGPCHPTLRG---GRLEKKSLSLPPYGLGCK 166  
 QY 180 --MVA-----HMVSGVFO--ATVNLGPEDEWRPHVWYGMFAFYAMLSFTCCMASAVTT 229  
 DB 167 NEMVLPGNADHHRSHISQLPATYRLATH-WBPCW-----AQBERLCCC----- 211  
 QY 230 FNTYTRMVLFEFKCKSKSPKENPN---CLPHHQCFFRRSLSSAA-----PTVGPLTSYH 280  
 DB 212 -----FLCPVRSPODGGPHDVFTSLPDCQLGSRRLRTTCLBLWLGILHGLALLH 261  
 QY 281 Q-----YHNPPIHSVSEV 294  
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## RESULT 14

US-09-990-456-272

; Sequence 272, Application US/09990456

; Patent No. US20020137890A1

; GENERAL INFORMATION:

APPLICANT: Aahkenazi, Avi J.  
 APPLICANT: Baker, Kevin P.  
 APPLICANT: Botstein, David  
 APPLICANT: Desnoyers, Luc  
 APPLICANT: Baton, Dan L.  
 APPLICANT: Ferrara, Napoleone  
 APPLICANT: Fong, Sherman  
 APPLICANT: Gerber, Hanspeter  
 APPLICANT: Gerritsen, Mary E.  
 APPLICANT: Goddard, Audrey  
 APPLICANT: Godowski, Paul J.  
 APPLICANT: Grimaldi, J. Christopher  
 APPLICANT: Gurney, Austin L.  
 APPLICANT: Kljavin, Ivar J.  
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 APPLICANT: Pan, James  
 APPLICANT: Paoni, Nicholas F.  
 APPLICANT: Roy, Margaret Ann  
 APPLICANT: Stewart, Timothy A.  
 APPLICANT: Tumas, Daniel  
 APPLICANT: Watanabe, Colin K.  
 APPLICANT: Williams, P. Mickey  
 APPLICANT: Wood, William I.  
 APPLICANT: Zhang, Zemin

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; PRIOR FILING DATE: 1998-07-09
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Matches 165; Conservative 14; Mismatches 76; Indels 65; Gaps 11;
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; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Deonoyers, Inc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Hong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Geriltsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
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; APPLICANT: Grimaldi, J. Christopher
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; APPLICANT: Kijavini, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
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; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tamas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
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 QY 61 MPVSLDGDNTSTQEVYQVNMETGDRFSFRSGMWLSCERTVEBPGRCRSPFLETP 120  
 61 MPVSLDGDNTSTQEVYQVNMETGDRFSFRSGMWLSCERTVEBPGRCRSPFLETP 120  
 QY 121 PAKREILWLSLGTQIYIIGIOPISFLLLDLLTGNPACGLSAPAVSSVLSGLG- 179  
 121 PAKREILWLSLGTQIYIIGIOPISFLLLDLLTGNPACGLSAPAVSSVLSGLG- 179  
 QY 180 --MVA-----HMVYSGVFO---ATVNIAGPEWREPHVYNYGMVYMWLSTFCMASAVTT 229  
 180 --MVA-----HMVYSGVFO---ATVNIAGPEWREPHVYNYGMVYMWLSTFCMASAVTT 229  
 QY 167 NPMVITGNDHLHRTIHLPTATNRLATN-WEPCLM-----AQTRILCCC----- 211  
 167 NPMVITGNDHLHRTIHLPTATNRLATN-WEPCLM-----AQTRILCCC----- 211  
 QY 230 FNTYTMVLBFKCKSKSKSPKRNPN---CLPHHQCPRRLSAA-----PTVGPILTSYH 280  
 230 FNTYTMVLBFKCKSKSKSPKRNPN---CLPHHQCPRRLSAA-----PTVGPILTSYH 280  
 QY 281 Q-----YANOPHSVSGV 294  
 281 Q-----YANOPHSVSGV 294  
 QY 262 LKHGVCCHLQVHVDGAGV 281  
 262 LKHGVCCHLQVHVDGAGV 281

Search completed: July 14, 2005, 20:37:53  
 Job time : 102.919 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: July 14, 2005, 20:14:28 ; Search time 22.3832 Seconds

(without alignments)  
1401.351 Million cell updates/sec

Title: US-10-019-151C-3

Perfect score: 1738  
Sequence: 1 MAKRELSKARSGCRTLISAI.....RGASQELKAVRSVEREQ 326

Scoring table:

BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

1: PIR.79:\*  
2: p1r1:\*  
3: p1r2:\*  
4: p1r3:\*  
4: p1r4:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	100.5	5.8	519	2 T15364	hypothetical prote
2	100.5	5.8	650	2 JC7088	heat shock protein
3	95	5.5	512	2 H84698	hypothetical prote
4	93.5	5.4	641	2 B45871	dnak-type molecula
5	92.5	5.3	641	2 S41415	hypothetical prote
6	92	5.3	585	2 S74477	hypothetical prote
7	91.5	5.3	636	2 T45468	dnak-type molecula
8	91	5.2	847	2 T04772	hypothetical prote
9	90.5	5.2	641	2 T49762	dnak-type molecula
10	89.5	5.1	465	2 T07620	dnak-type molecula
11	89	5.1	639	2 JC1391	dnak-type molecula
12	88.5	5.1	641	2 T45462	dnak-type molecula
13	88.5	5.1	642	2 JH0095	dnak-type molecula
14	88.5	5.1	646	2 S31716	dnak-type molecula
15	88.5	5.1	646	2 A27077	dnak-type molecula
16	88.5	5.1	646	2 JC4853	dnak-type molecula
17	88.5	5.1	646	2 A45935	dnak-type molecula
18	88.5	5.1	646	2 S07217	dnak-type molecula
19	88.5	5.1	650	2 S11456	dnak-type molecula
20	87.5	5.0	647	2 HXL170	dnak-type molecula
21	86.5	5.0	208	2 B44261	dnak-type molecula
22	86.5	5.0	340	2 H71479	probable outer mem
23	86.5	5.0	1240	2 T18393	lactophilin-3, spt
24	86.5	5.0	1308	2 T18408	lactophilin-3, spt
25	86	4.9	415	2 T24307	hypothetical prote
26	85.5	4.9	266	2 T12481	hypothetical prote
27	85.5	4.9	278	2 T15144	dnak-type molecula
28	85.5	4.9	461	1 OX14M	NADH2 dehydrogenas
29	85.5	4.9	467	2 T45479	heat-shock protein

30	85.5	4.9	640	1 HHK47A	dnak-type molecula
31	85.5	4.9	640	2 T21384	hypothetical prote
32	84.5	4.9	192	1 B64087	lipoprotein B - Ha
33	84.5	4.9	469	2 T45478	heat-shock protein
34	84.5	4.8	641	2 S35718	dnak-type molecula
35	84	4.8	375	2 S63685	neuropeptide Y rec
36	83.5	4.8	641	2 JN0668	dnak-type molecula
37	83.5	4.8	855	2 JH0287	immune regulatory
38	83.5	4.8	4872	2 S27272	ryanodine receptor
39	83	4.8	313	2 T05139	hypothetical prote
40	83	4.8	365	1 SAVLWR	large surface anti
41	83	4.8	565	2 P84721	probable RING zinc
42	83	4.8	650	2 S14949	dnak-type molecula
43	82.5	4.7	658	2 AC0379	DNA-directed DNA p
44	82	4.7	217	2 T24520	hypothetical prote
45	82	4.7	360	2 T11067	ubiquitinol-cytochro

#### ALIGNMENTS

##### RESULT 1

T15364 hypothetical protein C01C10.1 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C>Date: 20-Sep-1999 #sequence\_revision 20-Sep-1999 #text\_change 04-Mar-2000

C:Accession: T15364

R:Pauley, A.

submitted to the EMBL Data Library, March 1995

A:Description: The sequence of C. elegans cosmid C01C10.

A:Reference number: Z18337

A:Accession: T15364

A:Status: preliminary; translated from GB/EMBL/DD8J

A:Molecule type: DNA

A:Residues: 1-519 <PAU>

A:Cross-reference: EMBL:U23526; NID:9746577; PID:9746578; PIDN:AA836848.1; GSPDB:GN000

A:Experimental source: strain Bristol N2; clone C01C10

C:Genetics:

A:Gene: CESP:C01C10.1

A:Map position: X

A:Insertions: 30/3; 52/2; 86/1; 133/1; 164/3; 212/3; 250/3; 274/3; 313/3; 385/1; 415/3; 48

C:Superfamily: Caenorhabditis elegans hypothetical protein C01C10.1

Query Match 5.8%; Score 100.5; DB 2; Length 519;

Best Local Similarity 19.4%; Pred. No. 0.26;

Matches 50; Conservative 58; Mismatches 99; Indels 51; Gaps 10;

QY	81	WETGDRFRSPRSGMWTSCERTV-----BGRKRSFELTPAKREIL 127
DB	273	WQVADLDADRYVQSGIMLYCPQAOQCWTFPSDLINYTEKVDVCRFF--LIGDCRKLL 330
QY	128	-----W--LSAQITTYIGQIFSLTLTDLTLTGNPAGCLKLSAFAAVSVLSGL 177
DB	331	RTYPPFGMHAVALINLVISWICMSLCAAVTFYVVPARSRISVIMDVAFGASLL-C 389
QY	178	LGVAHAMTISQVQATVNLGPEBDMRPVWNYGAFTPAATLSFTCCMAAVTFR-----NT 232
DB	390	VSLIVFMVNAEMESKTLIGIKN--TYEKYGVSYVLAGIAF--VYSVTIVFAALVST 444
QY	233	YTFMVL-----FKCKSKSPKSNPNCLPHHOCFPRRLSAAPTVGRPLSYHQYN 284
DB	445	YTLFPBEVADSYTLKMSNQPARYNNDLPQPYOPRMSQLSKMPLST-----BNGS 497
QY	285	QPIHSVSEGVDFYSBLRN 302
DB	498	YINGAISPQDFFKQTRH 515

##### RESULT 2

JC7088 heat shock protein 70 - Stylophora pistillata

C:Species: Stylophora pistillata

C>Date: 03-Dec-1999 #sequence\_revision 03-Dec-1999 #text\_change 09-Jul-2004

C:Accession: JCT088  
R:Tom, M.; Durek, U.; Yankelevich, I.; Bosch, T.C.G.; Rinkevich, B.  
Biochem. Biophys. Res. Commun. 262, 103-108, 1999  
A:Title: Molecular characterization of the first heat shock protein 70 from a reef coral  
A:Reference number: JCT088; PMID:99382249; PMID:10448076  
A:Accession: JCT088  
A:Molecule type: DNA  
A:Residues: 1-650 <TOM>  
A:Cross-references: UNIPROT:Q9U777; GB:AF152004; NID:g6465981; PIDN:AAF12746.1; PID:g646  
C:Genetics:  
A:Gene: hsp70  
C:Superfamily: heat shock protein 70  
C:Keywords: ATP; molecular chaperone

Query Match  
Best Local Similarity 26.8%; Pred. No. 0.34;  
Matches 33; Conservative 11; Mismatches 42; Indels 37; Gaps 3;

QY 186 YSQVFOATVN--LGPEDMRPHVWNYGMAYFAMVLSFTCCMASAVTTENTYTRAVLEPKCK 243  
DB 219 FFFVLTAGTHTLGGEDFDNRMYDY-----FVSDPKOK 251

QY 244 HSKSPKFNPCLPHHQCFPRLLSSAAPVGPLTYSYHQNOPHSVSEGVDFYSRLRK 303  
DB 252 HKKDLKTNPKSL-----RLKTKACERAKTLLSSNSQANVEIDSLFEGIDFYSRLTRA 303

QY 304 GFG 306  
DB 304 KFE 306

RESULT 3  
H84698  
Hypothetical protein At2g29650 [imported] - Arabidopsis thaliana  
C:Species: Arabidopsis thaliana (mouse-ear cress)  
C:Date: 02-Feb-2001 #sequence\_revision 02-Feb-2001 #text\_change 09-Jul-2004  
C:Accession: H84698  
R:Lin, X.; Kaul, S.; Roundley, S.D.; Shea, T.P.; Bentro, M.T.; Town, C.D.; Fujii, C.Y.;  
M.; Koo, H.; Mofatt, K.S.; Cronin, L.A.; Shen, M.; Valtsen, S.E.; Umayam, L.; Talton, L.;  
euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.  
Nature 402, 761-768, 1999  
A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.  
A:Reference number: A84420; PMID:20083487; PMID:10617197  
A:Accession: H84698  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-512 <STO>  
A:Cross-references: UNIPROT:O82390; GB:AB020093; NID:g3582333; PIDN:AAC35230.1; GSPDB:GN  
C:Genetics:  
A:Gene: At2g29650  
A:Map position: 2  
C:Superfamily: hexuronate transporter

Query Match  
Best Local Similarity 20.6%; Pred. No. 0.84;  
Matches 63; Conservative 41; Mismatches 100; Indels 102; Gaps 16;

QY 26 LSPSTGLSNVYFGTQKVPK-----LCEKGLAKCP-----MPVSLDGTNTS 72  
DB 84 VSDSPSISIVPMW-----EEPPKXWVTVLCPGSAFLCNDNRVMSIALIFMSAEYGMNPA 139

QY 73 TGVVGVNMTGDRGDFRFRSGMWLSCETVBBPGRSRFTLELPRAKRIILWLSIG 132  
DB 140 TGLIISGFFWG--YLLTQIAGIIV--ADTV--GGRKVLGP-----GVIMWSIA 182

QY 133 TQITTYGLQF--ISFLLLTDLTLTGN-----PACGLKLSAPAAVS-----VLSGI-LG 179  
DB 183 TITTPVAALGLGLYLLVRAFMGVGSGVAMPANNNILSKVPPQBSRSRLALVYSGWYLG 242

QY 180 MVAHMYTSQVFOATVNLGPEDMRPHVWNYGM--AFY-----MAVLSFTCCMASAVTTN 231  
DB 243 SYTGIAFSFPL-----IHQFGMPGVFYSFGSIGTVMTL----- 276

QY 232 TYTRVLEFKCKSKSPKFNPCLPHH-----OCFPRLLSSAAPVGPLTS 278  
DB 277 -----MLTAAESSPLEDPILLBERKLTADNCASKSPKVSIPWRLTSLSPYVALIS 328

QY 279 YHQYHN 284  
DB 329 CHFCHN 334

RESULT 4  
B45871  
dnaK-type molecular chaperone HSP70-Hom - human  
N:Alternate names: heat shock protein HSP70-Hom  
C:Species: Homo sapiens (man)  
C:Date: 03-Mar-1994 #sequence\_revision 03-Mar-1994 #text\_change 09-Jul-2004  
C:Accession: B45871  
R:Milner, C.M.; Campbell, R.D.  
Immunogenetics 32, 242-251, 1990  
A:Title: Structure and expression of the three hrc-linked HSP70 genes.  
A:Reference number: A45871; PMID:91055806; PMID:1700760  
A:Accession: B45871  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-641 <ML>  
A:Cross-references: UNIPROT:P34931; GB:M59829; GB:M34268; NID:g188491; PIDN:AAA63228.1;  
C:Function:  
A:Description: involved in protein folding and assembling/disassembling of protein compl  
C:Superfamily: heat shock protein 70  
C:Keywords: ATP; molecular chaperone

Query Match  
Best Local Similarity 27.7%; Pred. No. 1.5;  
Matches 26; Conservative 15; Mismatches 38; Indels 15; Gaps 2;

QY 234 TRVLEFKCKSKSPKFNPCLPHHQCFPRLLSSAAPVGPLTYSYHQNOPHSVSEG 293  
DB 241 SHFVEFKKHKKKDKDISQNRVAV-----RLRTACERAKRTLLSSSQANLEIDSLYBG 292

QY 294 VDFYSRLRKNGFQ-----RGASQELKAVVSS 320  
DB 293 IDFTYSITRAREBELCADLFGTLERVERALRDA 326

RESULT 5  
S41415  
dnaK-type molecular chaperone Hsp70.3 - rat  
N:Alternate names: heat shock protein 70  
C:Species: Rattus norvegicus (Norway rat)  
C:Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 09-Jul-2004  
C:Accession: S41415; I68987  
R:Jutz, W.  
Submitted to the EMBL Data Library, January 1994  
A:Reference number: S41415  
A:Accession: S41415  
A:Molecule type: DNA  
A:Residues: 1-641 <LUT>  
A:Cross-references: UNIPROT:P55063; EMBL:X77209; NID:g1814002; PIDN:CAA54424.1; PID:g450  
Immunogenetics 40, 325-330, 1994  
A:Title: Comparative analysis of the three major histocompatibility complex-linked heat  
A:Reference number: I54542; PMID:95012453; PMID:7927536  
A:Accession: I68987  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-641 <RES>  
A:Cross-references: EMBL:X77209; NID:g1814002; PIDN:CAA54424.1; PID:g450934  
C:Genetics:  
A:Gene: Hsp70-3  
C:Function:  
A:Description: involved in protein folding and assembling/disassembling of protein compl  
C:Superfamily: heat shock protein 70  
C:Keywords: ATP; molecular chaperone



Immunogenetics 40, 159-162, 1994  
 A:Title: Coding sequences and levels of expression of Hsc70c are identical in mice with  
 A:Reference number: 149761; PMID:9429288; PMID:8026864  
 A:Accession: 149761  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: DNA  
 A:Residues: 1-641 <RES>  
 A:Cross-references: UNIPROT:P16627; GB:I27086; NID:g457299; PIDN:AAA5362.1; PID:g457300  
 C:Genetics:  
 A:Gene: Hsc70c  
 C:Function:  
 A:Description: involved in protein folding and assembling/dissassembling of protein comp1  
 C:Superfamily: heat shock protein 70  
 C:Keywords: ATP; molecular chaperone

Query Match 5.2%; Score 90.5; DB 2; Length 641;  
 Best Local Similarity 26.6%; Pred. No. 2.9;  
 Matches 25; Conservative 16; Mismatches 38; Indels 15; Gaps 2;

QY 234 TMVLEFKCKHSPKFNENCLPHHQCPRRLSSAAPVGLTSHQYHNPISHVSGVDFY 293  
 DB 241 SHFVEFFKKKKKKDKDISQNKRAV-----RRLRTACERAKRTLSSTQANLEIDSLYEG 292  
 QY 294 VDFYSELRNKGFQ-----RGASQELKEAVRS 320  
 DB 293 IDFTSITRAPEBELCADLFRGLTLEPEVEKSLRDA 326

RESULT 10  
 T07620  
 dnak-type molecular chaperone hsp70 - Cyanophora paradoxa (fragment)  
 C:Species: Cyanophora paradoxa  
 C:Date: 13-Aug-1999 #sequence\_revision 13-Aug-1999 #text\_change 09-Jul-2004  
 C:Accession: T07620  
 R:Reming, S.A.; Obdrlik, P.; Rober-Kleber, N.; Mueller, S.B.; Hofmann, C.J.; van de Pee  
 Bur, J. Physiol. 32, 279-288, 1997  
 A:Title: Molecular phylogeny of the stress-70 protein family with certain emphasis on al  
 A:Reference number: Z16057  
 A:Accession: T07620  
 A:Status: translated from GB/EMBL/DBJ  
 A:Molecule type: mRNA  
 A:Residues: 1-465 <REN>  
 A:Cross-references: UNIPROT:P93662; EMBL:X90949  
 A:Genetics:  
 A:Gene: hsp70  
 C:Function:  
 A:Description: involved in protein folding and assembling/dissassembling of protein comp1  
 C:Superfamily: heat shock protein 70  
 C:Keywords: ATP; molecular chaperone

Query Match 5.1%; Score 89.5; DB 2; Length 465;  
 Best Local Similarity 24.8%; Pred. No. 2.5;  
 Matches 33; Conservative 17; Mismatches 40; Indels 43; Gaps 4;

QY 195 NIGPEDMRPHVWNYGMAFYMAWLSFTCCMASAVTTENTYTRMVLSEFKCKHSPKFNENCL 254  
 DB 48 HIGGEFDPRMNVY-----FQGEKKKKKKDKDISQNKRAV 80  
 QY 255 LPHHQCPRRLSSAAPVGLTSHQYHNPISHVSGVDFYSELRNKGFQ-----R 307  
 DB 81 L-----RRLRTACERAKRTLSSTQANLEIDSLYEGIDFVATITRAKFEELNIDLR 131  
 QY 308 GASQELKEAVRS 320  
 DB 132 GCLPEVEKSLRDA 144

RESULT 11  
 JCI391  
 dnak-type molecular chaperone 701V - sea urchin (Paracentrotus lividus)  
 N:Alternat names: heat shock protein 701V; hsp701V protein  
 C:Species: Paracentrotus lividus (common urchin)  
 C:Date: 10-Jun-1993 #sequence\_revision 10-Jun-1993 #text\_change 09-Jul-2004

C:Accession: JCI391  
 R:Sconzo, G.; Scardina, G.; Ferraro, M.G.  
 Gene 121, 353-358, 1992  
 A:Title: Characterization of a new member of the sea urchin Paracentrotus lividus hsp70  
 A:Reference number: JCI391; PMID:93077053; PMID:1339375  
 A:Accession: JCI391  
 A:Molecule type: DNA  
 A:Residues: 1-639 <SCO>  
 A:Cross-references: UNIPROT:Q06248; EMBL:X61379; NID:g312916; PIDN:CAA43653.1; PID:g3129  
 C:Genetics:  
 A:Gene: hsp701V  
 A:Introns: 61/2  
 C:Function:  
 A:Description: involved in protein folding and assembling/dissassembling of protein comp1  
 C:Superfamily: heat shock protein 70  
 C:Keywords: ATP; heat shock; molecular chaperone; stress-induced protein

Query Match 5.1%; Score 89; DB 2; Length 639;  
 Best Local Similarity 31.9%; Pred. No. 4;  
 Matches 22; Conservative 10; Mismatches 29; Indels 8; Gaps 1;

QY 238 LEFKCKHSPKFNENCLPHHQCPRRLSSAAPVGLTSHQYHNPISHVSGVDFY 297  
 DB 243 LEFKKKKKKKDKDISQNKRAV-----RRLRTACERAKRTLSSTQANLEIDSLYEGIDFV 294  
 QY 298 SELRNKGFQ 306  
 DB 295 TISIRARPE 303

RESULT 12  
 I54542  
 dnak-type molecular chaperone HSP70 - rat  
 N:Alternat names: dnak-type molecular chaperone HSP70D; heat shock protein 70  
 C:Species: Rattus norvegicus (Norway rat)  
 C:Date: 02-Aug-1996 #sequence\_revision 02-Aug-1996 #text\_change 09-Jul-2004  
 C:Accession: I54542; I68986; S43388; S47522; I56574; S35955; S38199; S41413; S41414  
 R:Waler, L.; Rauh, F.; Gunther, B.  
 Immunogenetics 40, 325-330, 1994  
 A:Title: Comparative analysis of the three major histocompatibility complex-linked heat  
 A:Reference number: I54542; PMID:95012453; PMID:7927536  
 A:Accession: I54542  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: DNA  
 A:Residues: 1-641 <NAL1>  
 A:Cross-references: UNIPROT:Q07439; UNIPROT:Q63256; EMBL:X77207; NID:g1814000; PIDN:CAA5  
 A:Experimental source: HSP70.1  
 A:Genetics: HSP1  
 A:Accession: I68986  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: DNA  
 A:Residues: 1-641 <NAL2>  
 A:Cross-references: EMBL:X77208; NID:g927512; PIDN:CAA54423.1; PID:g450932  
 A:Experimental source: HSP70.2  
 A:Genetics: HSP2  
 R:Weserli, R.; Chi, S.H.; Sayen, M.R.; Dillmann, W.H.  
 Biochem. J. 298, 561-569, 1994  
 A:Title: Isolation of a novel inducible rat heat-shock protein (HSP70) gene and its expr  
 A:Reference number: S43388; PMID:94190258; PMID:8141767  
 A:Accession: S43388  
 A:Molecule type: DNA  
 A:Residues: 1-670, 'NG', '73-109', 'K', '111-203', 'R', '205-261', 'P', '263', 'ADGV', '268-641 <MES>  
 A:Cross-references: EMBL:X75557; NID:g407163; PIDN:CAA51140.1; PID:g407164  
 A:Experimental source: Ischaemic rat heart  
 R:Libowska, K.; Widiak, W.; Krawczyk, Z.; Wolniczke, P.; Wisniewski, J.  
 Biochim. Biophys. Acta 1219, 64-72, 1994  
 A:Title: Cloning, nucleotide sequence and expression of rat heat inducible hsp70 gene.  
 A:Reference number: S47522; PMID:94368874; PMID:8086479  
 A:Accession: S47522  
 A:Molecule type: DNA  
 A:Residues: 1-70, 'NG', '73-407', 'A', '409-641 <LIS>  
 A:Cross-references: EMBL:X74271; NID:g3413498; PIDN:CAA52328.1; PID:g396270  
 A:Note: the authors translated the codon CCG for residue 365 as Asp

```

R.Longo, F.M.; Wang, S.J.; Narasimhan, P.; Zhang, J.S.; Chen, J.; Maasa, S.M.; Sharp, F.R.
J. Neurosci., Res. 36, 325-335, 1993
A.Title: cDNA cloning and expression of stress-inducible rat hsp70 in normal and injured
A.Reference number: I56574; MUID:94096443; PMID:8271311
A.Accession: I56574
A.Status: preliminary; translated from GB/EMBL/DBJ
A.Molecule type: mRNA
A.Residues: 1-226 /D/, 228-641 <LON>
A.Cross-references: GB:I16764; NID:G294567; PIDN:AAI17441.1; PID:G294568
C.Genetics: <HSP1>
A.Gene: hsp70.1
C.Genetics: <HSP2>
A.Gene: hsp70.2
C.Function:
A.Description: Involved in protein folding and assembling/disassembling of protein comp
C_SUPERfamily: heat shock protein 70
C.Keywords: ATP; heat shock; molecular chaperone; stress-induced protein

Query Match          5.1% Score 88.5; DB 2; Length 641;
Best Local Similarity 26.6%; Pred. No. 4.5;
Matches 25; Conservative 16; Mismatches 38; Indels 15; Gaps 2;

Oy      234 TRWVLEPKCKGSKSFKENPNCLPHHQCFPRRLSSAAPVGPVTSYHOYNQPIHSVSG 293
         |||||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db      239 SHVEVEPKRKHKKDIGNKAV-----RRLRACERAKRTLSSTQASLEIDSLEFG 290
         :|||||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|

Oy      294 VDFYSELRNKGFO-----RGASQQLKEAVRSS 320
         :|||::|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db      291 IDFYTSITRARFELCSDLFRGTLEPVEKALRDA 324
         :|||::|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|

RESULT 14
S31716
dnaK-type molecular chaperone hsp72-pel - rat
C.Species: Rattus norvegicus (Norway rat)
C.Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 20-Aug-1999
C.Accession: I60329; S31716
C.Walter, L.; Heine, L.; Gunther, B.
immunogenetics 39, 351-354, 1994

```

```

A>Title: Sequence, expression, and mapping of a rat Mhc class Ib gene.
A|Reference number: |60329; MUID:94222444; PMID:7545923
A|Accession: |60329
A|Status: Preliminary; translated from GB/EMBL/DBJ
A|Molecule type: DNA
A|Residues: 1-646 <RES>
A|Cross-references: EMBL:X70065; NTD:g56384; PIDN:CAA49670.1; PID:g56385
C|Genetics:
A|Gene: hap72-psl
C|Function:
A|Description: Involved in protein folding and assembling/dissassembling of protein comp
C|Superfamily: heat shock protein 70
C|Keywords: ATP, molecular chaperone

Query Match          5.1%; Score 88.5; DB 2; Length 646;
Best Local Similarity 27.5%; Pred. No. 4.6;
Matches    25; Conservative   14; Mismatches   37; Indels    15; Gaps     2;

QY      237 VLEFKCKSKSPKENPCLPHHQCPRRLSSAAPVTPLSYHYQHNPISHVSEGVDF 296
        : ||||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : |||
Db       242 IAEFRKRRKKDKISENKRAV-----RRLRTACERARRTLSSSTQASIEIDSLYEIGDIF 293
               :           :         :         :         :         :         :         :         :         :
QY      297 YSELRNKGFO-----RGASQLKEAVRSS 320
        |: : : |: : : |: : : |: : : |: : : |: : : |: : : |: : : |: : : |: : :
Db       294 YTSITRARFBEINADLFRTGLDPVEKALRDA 324
               : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 15
A27077
dnak-type molecular chaperone - human
M|Alternate names: heat shock cognate protein 70
C|Species: Homo sapiens (man)
C|Date: 19-Nov-1988 #sequence_revision 19-Nov-1988 #text_change 09-Jul-2004
C|Accession: A27077
R:Dworniczak B.; Mirault M.B.
Nucleic Acids Res. 15, 5181-5197, 1987
A>Title: Structure and expression of a human gene coding for a 71 kd heat shock 'cognat
A|Reference number: A27077; MUID:87259994; PMID:3037489
A|Accession: A27077
A|Molecule type: DNA
A|Residues: 1-646 <DMO>
A|Cross-references: UNIPROT:P11142; GB:M19141
C|GeneticS:
A|Introns: 69/1; 137/3; 188/3; 374/1; 441/3; 508/1; 585/3
C|Function:
A|Description: involved in protein folding and assembling/disassembling of protein comp
C|Superfamily: heat shock protein 70
C|Keywords: ATP, molecular chaperone

Query Match          5.1%; Score 88.5; DB 2; Length 646;
Best Local Similarity 27.5%; Pred. No. 4.6;
Matches    25; Conservative   14; Mismatches   37; Indels    15; Gaps     2;

QY      237 VLEFKCKSHSPKENPNCLPHHQCPRRLSSAAPVTGPTLSYHQYNQPISHVSSEGVDF 296
        : ||||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : |||
Db       242 IAEFRKRRKKDKISENKRAV-----RRLTACERARRTLSSSTQASIEIDSLYEIGDIF 293
               :           :         :         :         :         :         :         :         :         :
QY      297 YSELRNKGFO-----RGASQLKEAVRSS 320
        |: : : |: : : |: : : |: : : |: : : |: : : |: : : |: : : |: : : |: : :
Db       294 YTSITRARFBEINADLFRTGLDPVEKALRDA 324
               : : ~ : : : : : : : : : : : : : : : : : : : : : :

Search completed: July 14, 2005, 20:33:22
Job time : 28.3832 secs
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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: July 14, 2005, 19:55:46 ; Search time 102.168 Seconds  
(without alignments)  
1633.949 Million cell updates/sec

Title: US-10-019-151C-3

Perfect score: 1738

Sequence: 1 MAMMELSKAFSGQRTLLSAT.....RGASQELKAVRSVSEEC 326

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Uniprot 03:\*  
1: uniprot\_sprot:\*  
2: uniprot\_tramb1.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1733	99.7	326	2 Q8NBR4	Q8NBR4 homo sapien
2	1718	98.8	323	2 Q8NBR4	Q8NBR4 homo sapien
3	1450.5	83.5	275	2 Q8NBS0	Q8NBS0 mus sapien
4	1249.5	71.9	365	2 Q8R1W2	Q8R1W2 mus musculi
5	1214.5	69.9	366	2 Q6AYL2	Q6AYL2 rattus norv
6	987.5	56.8	343	2 Q8NBR1	Q8NBR1 homo sapien
7	887.5	51.1	304	2 Q9Z1H7	Q9Z1H7 mus musculi
8	789.5	45.4	217	2 Q9D9Z3	Q9D9Z3 mus musculi
9	785.5	45.2	217	2 Q8C2N5	Q8C2N5 mus musculi
10	657.5	37.8	285	2 Q9B8I6	Q9B8I6 homo sapien
11	643.5	37.0	282	2 Q9BUT4	Q9BUT4 mus sapien
12	623	35.8	326	2 Q9GLP9	Q9GLP9 mus sapien
13	531	30.6	280	2 Q6UXI4	Q6UXI4 homo sapien
14	366	21.1	194	2 Q7Z6F8	Q7Z6F8 homo sapien
15	365.5	21.0	176	2 Q8T8B1	Q8T8B1 homo sapien
16	348	20.0	175	2 Q6DD55	Q6DD55 xenopus lae
17	111	6.4	314	2 Q98UH4	Q98UH4 gallus gall
18	108.5	6.2	315	1 CCG3 HUMAN	C60359 homo sapien
19	108.5	6.2	328	2 Q90X18	Q90X18 gallus gall
20	107.5	6.2	327	1 CCG4 RAT	Q8VW9 rattus norv
21	106.5	6.1	327	1 CCG4 MOUSE	Q9J1V4 mus musculi
22	105.5	6.0	315	1 CCG3 RAT	Q8VH0 rattus norv
23	104.5	6.0	607	1 VBI HPV24	P50762 human papil
24	104	6.0	203	1 CLDM HUMAN	Q8N73 homo sapien
25	104	6.0	327	1 CCG4 HUMAN	Q8VH1 homo sapien
26	103	5.9	512	2 Q8K4H0	Q8V40 arabis dopsis
27	102.5	5.9	250	2 Q8U7F8	Q8J1F8 fugu rubrip
28	102	5.9	323	2 Q99PR9	Q99PR9 rattus norv
29	100.5	5.8	165	1 NKG7 MOUSE	Q99P5 mus musculi
30	100.5	5.8	275	1 Q6GM02	Q6GM02 xenopus lae
31	100.5	5.8	281	1 CLC5_CAMEL	Q9NGJ7 caenorhabdi

32	100.5	5.8	323	1 CCG2 HUMAN	Q9V698 homo sapien
33	100.5	5.8	650	2 Q9U777	Q9U777 stylophora
34	99.5	5.7	165	2 Q9CY55	Q9CY55 mus musculi
35	99.5	5.7	315	1 CCG3 MOUSE	Q9J1V5 mus musculi
36	99	5.7	191	2 Q6B568	Q6B568 fugu rubrip
37	99	5.7	323	1 CCG2 MOUSE	Q8B602 mus musculi
38	99	5.7	323	2 Q71R72	Q71R72 rattus norv
39	98.5	5.7	190	2 Q6B5P1	Q6B5P1 fugu rubrip
40	98.5	5.7	443	2 Q6N218	Q6N218 rhodosphe
41	98	5.6	275	2 Q8R410	Q8R410 mus musculi
42	96	5.5	275	1 CCG5 MOUSE	Q8VH4 mus musculi
43	96	5.5	275	1 CCG5 RAT	Q8VH8 rattus norv
44	95.5	5.5	220	1 CLDM MOUSE	Q9D7U6 mus musculi
45	95.5	5.5	324	2 Q6PFS3	Q6PFS3 brachydanto

## ALIGNMENTS

RESULT 1	Q8NBR4	P8R1MINARY;	PRT;	326 AA.
AC	Q8NBR4			
DT	01-OCT-2002 (T8EMBLrel. 22, Created)			
DT	01-OCT-2002 (T8EMBLrel. 22, Last sequence update)			
DT	01-OCT-2002 (T8EMBLrel. 22, Last annotation update)			
DS	Hypothetical protein FLJ90841.			
OS	Homo sapiens (Human)			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RA	Isoogl T., Oca T., Nishikawa T., Hayaishi K., Otsuki T., Sugiyama T.,			
RA	Suzuki Y., Nagai K., Sugano S., Ishii S., Kawai-Hio Y., Saito K.,			
RA	Yamamoto J., Wakamatsu A., Nakamura Y., Kojima S., Nagahara K.,			
RA	Masuno Y., Ono T., Okano K., Yoshikawa Y., Aotsuka S., Saeki K.,			
RA	Hacori A., Okumura K., Iwayanagi T., Ninomiya K.,			
RL	Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.			
DR	EMBL; AK075322; BAC11548.1; -			
SQ	SEQUENCE 326 AA; 36751 MW; 9A9682984F6B6D06 CRC64;			
Query Match	99.7%; Score 1733; DB 2; Length 326;			
Best Local Similarity	99.7%; Pred. No. 4.4e-147;			
Matches 325; Conservative	0; Mismatches 1; Indels 0; Gaps 0;			
QY	1 MAMMELSKAFSGQRTLLSATLSMLSLSPFTTSLSNYMFVGTQKVPKPLCEKGLAAKCPD 60			
DB	1 MAMMELSKAFSGQRTLLSATLSMLSLSPFTTSLSNYMFVGTQKVPKPLCEKGLAAKCPD 60			
QY	61 MPVSLDGDNTSTQBVVQYVMEETGDRFSFRSFRSGMWLSCEBTEBGERCRSPFELTP 120			
DB	61 MPVSLDGDNTSTQBVVQYVMEETGDRFSFRSFRSGMWLSCEBTEBGERCRSPFELTP 120			
QY	121 PARREILMLSLGQITTYIGQIFSPILLTDLTLTENPACGLSLSPAANVSSTLSGLGM 180			
DB	121 PARREILMLSLGQITTYIGQIFSPILLTDLTLTENPACGLSLSPAANVSSTLSGLGM 180			
QY	121 PARREILMLSLGQITTYIGQIFSPILLTDLTLTENPACGLSLSPAANVSSTLSGLGM 180			
DB	121 PARREILMLSLGQITTYIGQIFSPILLTDLTLTENPACGLSLSPAANVSSTLSGLGM 180			
QY	181 VAHMTSOFVQATVNLGPEDMRPHVMNYGAFYAMLSFTCCNAAVATTTNTTNTVLEF 240			
DB	181 VAHMTSOFVQATVNLGPEDMRPHVMNYGAFYAMLSFTCCNAAVATTTNTTNTVLEF 240			
QY	241 KCHGHSFKENPNCLEPHHQCCEPRRLSSAAPTGVPTSTYHQYNQPIHVSSEGVDFSEL 300			
DB	241 KCHGHSFKENPNCLEPHHQCCEPRRLSSAAPTGVPTSTYHQYNQPIHVSSEGVDFSEL 300			
QY	301 RNKGFORGASQELKEAVRSVSEEC 326			
DB	301 RNKGFORGASQELKEAVRSVSEEC 326			
RESULT 2	Q8NBR4			

ID Q8N4M3 PRELIMINARY; PRT; 323 AA.  
AC Q8N4M3;  
DT 01-OCT-2002 (TrEMBLrel. 22, Created)  
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)  
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)  
DE GSG1 protein.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Brain;  
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Schuler G.D.,  
Klauser R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
Brownstein M.J., Uddin T.B., Tsohyukl S., Carninci P., Prange C.,  
Rana S.S., Loughlano N.A., Peters G.J., Abramson R.D., Mullany S.J.,  
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
Richard S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
Vallalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
Fahy J., Helton E., Kettelman M., Madan A., Rodriguez Y., Bouffard G.G.,  
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
Krzyszczak M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,  
Jones S.J., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
and mouse cDNA sequences";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
RP SEQUENCE FROM N.A.  
RC TISSUE=Brain;  
RA Strausberg R.;  
DR EMBL/BC033854; AAK33854.1; -.  
SQ SEQUENCE 323 AA; 36376 MW; 5FBEL3C21BF6C081 CRC64;  
Query Match 98.8%; Score 1718; DB 2; Length 323;  
Best Local Similarity 99.7%; Pred. No. 9,7e-146;  
Matches 322; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 4 MEISKAFGSQRITLSAIIISMLSISFSTTSLISNYWVGQVKPKICBKGIAKCFDMPV 63  
DB 1 MEISKAFGSQRITLSAIIISMLSISFSTTSLISNYWVGQVKPKICBKGIAKCFDMPV 60  
QY 64 SLDDGNTSTQEVVQYNWETGDRFSPFRSGMWLSCEETVEEPEBCRSFIELTPPAK 123  
DB 61 SLDDGNTSTQEVVQYNWETGDRFSPFRSGMWLSCEETVEEPEBCRSFIELTPPAK 120  
QY 124 REILMLSLGTQITTYIGLOFISFLILTDLLITGNPAAGLKLGAFAVSSVSLGLGMVAH 183  
DB 121 REILMLSLGTQITTYIGLOFISFLILTDLLITGNPAAGLKLGAFAVSSVSLGLGMVAH 180  
QY 184 MWYSQVFOATVNLGPEDMRPHVWNYGMAYMAVLSFTCCMASAVTTFTNTYRNVLEPKCK 243  
DB 181 MWYSQVFOATVNLGPEDMRPHVWNYGMAYMAVLSFTCCMASAVTTFTNTYRNVLEPKCK 240  
QY 244 HSKSFKENPNCLEPHHQCPRRLSSAAPTVPGLTSHQYHNPRIHVSSEGVDFYSELRLNK 303  
DB 241 HSKSFKENPNCLEPHHQCPRRLSSAAPTVPGLTSHQYHNPRIHVSSEGVDFYSELRLNK 300  
QY 304 GFORGASQELKEAVRSVVEEBC 326  
DB 301 GFORGASQELKEAVRSVVEEBC 323

ID Q8NBS0 PRELIMINARY; PRT; 275 AA.  
AC Q8NBS0;  
DT 01-OCT-2002 (TrEMBLrel. 22, Created)  
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)  
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)  
DE Hypothetical protein FLJ90830.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Isegai T., Ota T., Nishikawa T., Hayaehi K., Otsuki T., Sugiyama T.,  
Suzuki Y., Nagai K., Sugano S., Ishii S., Kawai-Hio Y., Saito K.,  
Yamamoto J., Wakamatsu A., Nakamura Y., Kojima S., Nagahara K.,  
Masuno Y., Ono T., Okano K., Yoshikawa Y., Aotsuba S., Sasaki N.,  
Hattori A., Okumura K., Iwayanagi T., Niimura Y. K.;  
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.  
DR EMBL/AK075311; BAC11540.1; -.  
SQ SEQUENCE 275 AA; 31300 MW; 503F7AC849CBEB9 CRC64;  
Query Match 83.5%; Score 1450.5; DB 2; Length 275;  
Best Local Similarity 84.0%; Pred. No. 8.3e-122;  
Matches 274; Conservative 1; Mismatches 0; Indels 51; Gaps 1;  
QY 1 MAKMEISKAFGSQRITLSAIIISMLSISFSTTSLISNYWVGQVKPKICBKGIAKCFD 60  
DB 1 MAKMEISKAFGSQRITLSAIIISMLSISFSTTSLISNYWVGQVKPKICBKGIAKCFD 60  
QY 61 MEVSLDGTNTSTQEVVQYNWETGDRFSPFRSGMWLSCEETVEEPEBCRSFIELTP 120  
DB 61 MEVSLDGTNTSTQEVVQYNWETGDRFSPFRSGMWLSCEETVEEPEBCRSFIELTP 120  
QY 121 PAKREILMLSLGTQITTYIGLOFISFLILTDLLITGNPAAGLKLGAFAVSSVSLGLGM 180  
DB 121 PAKR-----GLGM 129  
QY 181 VAHMWYSQVFOATVNLGPEDMRPHVWNYGMAYMAVLSFTCCMASAVTTFTNTYRNVLEF 240  
DB 130 VAHMWYSQVFOATVNLGPEDMRPHVWNYGMAYMAVLSFTCCMASAVTTFTNTYRNVLEF 189  
QY 241 KCKHSKSFENPNCLEPHHQCPRRLSSAAPTVPGLTSHQYHNPRIHVSSEGVDFYSEL 300  
DB 190 KCKHSKSFENPNCLEPHHQCPRRLSSAAPTVPGLTSHQYHNPRIHVSSEGVDFYSEL 249  
QY 301 RNKGFORGASQELKEAVRSVVEEBC 326  
DB 250 RNKGFORGASQELKEAVRSVVEEBC 275  
RESULT 4  
ID Q8RLW2 PRELIMINARY; PRT; 365 AA.  
AC Q8RLW2;  
DT 01-JUN-2002 (TrEMBLrel. 21, Created)  
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)  
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)  
DE Gag1 protein.  
GN Name=Gag1;  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Eye;  
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
Klauser R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,



RA Brownstein M.J., Uedlin T.B., Toshlyuk S., Carninci P., Prange C.,  
 RA Raba S.S., Loguallano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Wotley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahy J., Helton E., Kettman M., Madan A., Rodríguez S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
 RA Krzywinski M.I., Skalek U., Smallus D.E., Schnerch A., Schein J.E.,  
 RA Jones S.J., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 RT and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16699-16903(2002).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Eye;  
 RA Strausberg R.;  
 RL Submitted (FEb-2002) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; BC023009; AAH23009.1; -  
 DR MGD; MGI:1194499; Gggl.  
 DR GO; GO:0016021; C:Integral to membrane, TAS;  
 DR GO; GO:0016021; C:Integral to membrane, TAS;  
 DR SEQUENCE 365 AA; 40612 MW; 2D0A0AEC0BA971FD CRC64;  
 SQ  
 Query Match 71.9%; Score 1249.5; DB 2; Length 365;  
 Best Local Similarity 66.3%; Pred. No. 1.3e-103;  
 Matches 242; Conservative 25; Mismatches 55; Indels 43; Gaps 3;  
 QY 4 MELSKAFSGQRTLLSAILSMLSLSPSTSLSNYPVGTOKVPRKCEKGLAAKCFDMPV 63  
 DB 1 MEFQKSSDQRTFSAIINMLSLGLSTALSLSEMFVGAQKVPKPLCGSLAAKCFDMPM 60  
 QY 64 SLQGD-TNISTGVQVQVWETGDRFRFRSGMGLSCETVBERPGRSFTLETPPA 122  
 DB 61 SLQGIANTSAQVQVWETGDRFRFRSGMGLSCETVBERPGRSFTLETPPA 120  
 QY 123 KR-----ELWLSIGTQITTYGLQ 141  
 DB 121 QREKGLERATLQSGCHPTLRFGGEMEMASLILPMPGVAKVFWLSLGAQTAYIGLQ 180  
 QY 142 FISFLLLTDLLLTGNPACGLKLSAPAAVSVLSGLGNVAHMYSQVQATVNLGPEBW 201  
 DB 181 LISFLLLTDLLLTGNPGCLKLSAPAAVSVLSGLGNVAHMYLQVQATVNLGPEBW 240  
 QY 202 RPHVNTYGAFFYAAWLSFTCCMASAVTTFTYTRMTLEFRCKSKSPKPNCLPHNHOC 261  
 DB 241 RPHSNWYGAFFYAAWLSFTCCMASAVTTFTYTRMTLEFRCKSKSPKPNCLPHNHOC 300  
 QY 262 F-FPRRLSSAAPTGVGLTSYHYNOPTHSVSEGVDFVSELBNKGFQSGASOELKEAVRSS 320  
 DB 301 FLPPPLCTTHAGBPSSCHQPSHPTRSVSEALDYSLADKXFOQISQELKEVPEPS 360  
 QY 321 VEEBOC 325  
 DB 361 VEEBOC 365  
 RESULT 5  
 Q6AYL2 PRELIMINARY; PRT; 366 AA.  
 AC Q6AYL2;  
 DT 25-OCT-2004 (T-EMBLrel. 28, Created)  
 DT 25-OCT-2004 (T-EMBLrel. 28, Last sequence update)  
 DT 25-OCT-2004 (T-EMBLrel. 28, Last annotation update)  
 DE Hypochemical protein.  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 NC NCB1\_TaxID=10116;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Testis;  
 RX PubMed=12477932; DOI=10.1073/pnas.242603899;

RA Strausberg R.L., Feingold B.A., Grouse L.H., Derge J.G.,  
 RA Kuaner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Allecchi S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diatchenko L., Marisla K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Uedlin T.B., Toshlyuk S., Carninci P., Prange C.,  
 RA Raba S.S., Loguallano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Wotley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahy J., Helton E., Kettman M., Madan A., Rodríguez S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
 RA Krzywinski M.I., Skalek U., Smallus D.E., Schnerch A., Schein J.E.,  
 RA Jones S.J., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 RT and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16699-16903(2002).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Testis;  
 RA Director MGC Project;  
 RL Submitted (AUG-2004) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; BC079000; AAH79000.1; -  
 DR KW Hypothetical protein.  
 DR SEQUENCE 366 AA; 40559 MW; 20807F1B9567C494 CRC64;  
 SQ  
 Query Match 69.9%; Score 1214.5; DB 2; Length 366;  
 Best Local Similarity 65.4%; Pred. No. 1.8e-100;  
 Matches 240; Conservative 22; Mismatches 60; Indels 45; Gaps 4;  
 QY 4 MELSKAFSGQRTLLSAILSMLSLSPSTSLSNYPVGTOKVPRKCEKGLAAKCFDMPV 63  
 DB 1 MEFQKSSDQRTFSAIINMLSLGLSTALSLSEMFVGAQKVPKPLCGSLAAKCFDMPM 60  
 QY 64 SLQGD-TNISTGVQVQVWETGDRFRFRSGMGLSCETVBERPGRSFTLETPPA 122  
 DB 61 SLQGIANTSAQVQVWETGDRFRFRSGMGLSCETVBERPGRSFTLETPPA 120  
 QY 123 KR-----ELWLSIGTQITTYGLQ 141  
 DB 121 QREKGLERATLQSGCHPTLRFGGEMEMASLILPMPGVAKVFWLSLGAQTAYIGLQ 180  
 QY 142 FISFLLLTDLLLTGNPACGLKLSAPAAVSVLSGLGNVAHMYSQVQATVNLGPEBW 201  
 DB 181 LISFLLLTDLLLTGNPGCLKLSAPAAVSVLSGLGNVAHMYLQVQATVNLGPEBW 240  
 QY 202 RPHVNTYGAFFYAAWLSFTCCMASAVTTFTYTRMTLEFRCKSKSPKPNCLPHNHOC 261  
 DB 241 RPHSNWYGAFFYAAWLSFTCCMASAVTTFTYTRMTLEFRCKSKSPKPNCLPHNHOC 300  
 QY 262 F-FPRRLSSAAPTGVGLTSYHYNOPTHSVSEGVDFVSELBNKGFQSGASOELKEAVRSS 319  
 DB 301 FLPPPLCTTHAGBPSSCHQPSHPTRSVSEALDYSLADKXFOQISQELKEVPEPS 360  
 QY 320 VEEBOC 326  
 DB 361 SV-EEBOC 366  
 RESULT 6  
 Q8NBT1 PRELIMINARY; PRT; 343 AA.  
 AC Q8NBT1;  
 DT 01-OCT-2002 (T-EMBLrel. 22, Created)  
 DT 01-OCT-2002 (T-EMBLrel. 22, Last sequence update)  
 DT 01-MAR-2003 (T-EMBLrel. 23, Last annotation update)  
 DE Hypochemical protein (Human).  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.

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OX  NCBI_TaxId=9606;
RN  [1]
RP  SEQUENCE FROM N.A.
RA  Isegai T., Ota T., Nishikawa T., Hayaashi K., Otsuki T., Sugiyama T.,
RA  Suzuki Y., Nagai K., Sugano S., Ishii S., Kawai-Hio Y., Saito K.,
RA  Yamamoto J., Wakamatsu A., Nakamura Y., Kojima S., Nagahara K.,
RA  Masuhara Y., Ono T., Okano K., Yoshikawa Y., Aotaka S., Sasaki N.,
RA  Hattori A., Okumura K., Iwayanagi T., Niimiya K.,
RA  Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR  EMBL; AK075288; BAC11524.1; -.
DR  Genem; HGNC:19716; GSG1.
SQ  SEQUENCE 343 AA; 38154 MW; F71938F7435C3FC2 CRC64;

Query Match      56.8%; Score 987.5; DB 2; Length 343;
Best Local Similarity 61.9%; Pred. No. 4e-80;
Matches 226; Conservative 13; Mismatches 65; Indels 61; Gaps 13;

QY  1 MAKMEISKAFSGQRTLLSAILSMLSLSPSTTSLSNVYFVGQKVPKPLCEKGLAKCFD 60
    |||
DB  1 MAKMEISKAFSGQRTLLSAILSMLSLSPSTTSLSNVYFVGQKVPKPLCEKGLAKCFD 60

QY  61 MPVSLDGDNTNSTQEVVQYNNMETGDDRFSPFRSGMWLSCBETVEBGERCRSPFIELTP 120
    |||
DB  61 MPVSLDGDNTNSTQEVVQYNNMETGDDRFSPFRSGMWLSCBETVEBGERCRSPFIELTP 120

QY  121 PAKREILWLSLGTQIYIGLQIFISFLILLTDLLLTGNPACGLKLSAFAVSVLSGLLG- 179
    |||
DB  121 PAKRGEKGL-----LEFATLQGPCHPTLPFG---GKRLMEKASLSPSPILGLCGK 166

QY  180 --MVA-----HMVYSGVFQ---ATVNLGPEDMRPHVYNNYGMAYMAMLSFTCCMASAVTT 229
    |||
DB  167 NPVITIGNADHLHRTSTHQLPATNRLATN-WERCIM-----AQTERLCCCFELCPVNS 218

QY  230 -----FNTYTRNV-----LEFKC-----KHSSK---FKENPNC--LPH-HRQC 261
    |||
DB  219 PGDGGPHDVFTSLPSDCQLGSRRLFTTCLELMGLGLALHLHLGVCCHLQHVHQC 278

QY  262 PPRRLSSAAPTVGPTLSYHOYHNOPIHSSEGVDFPSELNKGFORGASQELKAVRSSV 321
    |||
DB  279 PPRRLSSAAPTVGPTLSYHOYHNOPIHSSEGVDFPSELNKGFORGASQELKAVRSSV 338

QY  322 EEEQC 326
    |||
DB  339 EEEQC 343

RESULT 7
Q921H7 PRELIMINARY; PRT; 304 AA.
AC  Q921H7;
DT  01-MAY-1999 (TrEMBLrel. 10, Created)
DT  01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT  01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE  GSG1.
GN  Mus musculus (Mouse).
OS  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC  Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX  NCBI_TaxId=10090;
RN  [1]
RP  SEQUENCE FROM N.A.
RA  STRAIN=Black 6; TISSUB=Testis; DOI=10.1016/0014-5793(94)01155-9;
RX  MEDLINE=95046372; PubMed=7957958;
RA  Tanaka H., Yoshimura Y., Nishina Y., Nozaki M., Nojima H.,
RA  Nishimune Y.,
RT  Isolation and characterization of cDNA clones specifically expressed
RT  in testicular germ cells."
RL  FEBS Lett. 355:4-10(1994).
RN  [2]
RP  SEQUENCE FROM N.A.
RA  STRAIN=Black 6; TISSUB=Testis;
RX  MEDLINE=98051916; PubMed=9337410;
RA  Matsui M., Ichihara H., Kobayashi S., Tanaka H., Tsuchida J.,

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RA  Nozaki M., Yoshimura Y., Nojima H., Rochelle J.M., Nishimune Y.,
RA  Takeo M.M., Seldin M.F.;
RT  Mapping of six germ-cell-specific genes to mouse chromosomes."
RL  Mamm. Genome 8:873-874(1997).
DR  EMBL; D87325; BAA37087.1; -.
DR  MGI; MGI:1194499; Gsg1.
DR  GO; GO:0016021; C:integral to membrane; TAS.
SQ  SEQUENCE 304 AA; 33454 MW; 8B19EF61CA5016 CRC64;

Query Match      51.1%; Score 887.5; DB 2; Length 304;
Best Local Similarity 61.3%; Pred. No. 3.3e-71;
Matches 185; Conservative 17; Mismatches 45; Indels 55; Gaps 5;

QY  4 MELSKAFSGQRTLLSAILSMLSLSPSTTSLSNVYFVGQKVPKPLCEKGLAKCFDMPV 63
    |||
DB  1 MEPOKSSDQRTFPISSAILSMLSLSPSTTSLSNVYFVGQKVPKPLCEKGLAKCFDMPV 60

QY  64 SLDDG-TNVTSTQEVVQYNNMETGDDRFSPFRSGMWLSCBETVEBGERCRSPFIELTP 122
    |||
DB  61 SLDDGANTSNABVQYTNWETGDDRFSPFLAFSGMWLSCBETVEBGERCRSPFIELTP 120

QY  123 KR-----
    |||
DB  121 QREKGLLEFATLQSGCHPTLPFGGEWLMKASLHLPLPWGPAKVPWLSLGAQTAYIGIQ 180

QY  142 FISPLILLTDLLLTGNPACGLKLSAFAVSVLSGLLGVAHMYSOVQATVNLGPE-- 199
    |||
DB  181 LISPLILLTDLLLTGNPACGLKLSAFAVSVLSGLLGVAHMYSOVQATVNLGPE-- 240

QY  200 ---DMRPHVNNYGMAYMAMLSFTCCMASAVTTENTYTRVWLEFKCRKSKSPKENPCL 255
    |||
DB  241 TLLELR-----LGLHSGFLHL--LHGVTYTTNMTTRVWLEFKCRKSKSFNTNPSCL 293

QY  256 PH 257
    |||
DB  294 AH 295

RESULT 8
Q992J3 PRELIMINARY; PRT; 217 AA.
AC  Q992J3;
DT  01-JUN-2001 (TrEMBLrel. 17, Created)
DT  01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT  01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE  Mus musculus adult male testis cDNA, RIKEN full-length enriched
DE  library, clone:170025C22 product:germ cell-specific gene 1, full
DE  insert sequence.
GN  Name=Gsg1;
OS  Mus musculus (Mouse).
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC  Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX  NCBI_TaxId=10090;
RN  [1]
RP  SEQUENCE FROM N.A.
RA  STRAIN=C57BL/6J; TISSUB=Testis;
RX  MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA  Carnucci P., Hayaishiaki Y.,
RT  "High-efficiency full-length cDNA cloning."
RL  Meth. Enzymol. 303:19-44(1999).
RN  [2]
RP  SEQUENCE FROM N.A.
RA  STRAIN=C57BL/6J; TISSUB=Testis;
RX  MEDLINE=21085600; PubMed=11217851; DOI=10.1038/35055500;
RA  RIKEN FANTOM Consortium;
RT  "Functional annotation of a full-length mouse cDNA collection."
RL  Nature 409:685-690(2001).
RN  [3]
RP  SEQUENCE FROM N.A.
RA  STRAIN=C57BL/6J; TISSUB=Testis;
RX  The FANTOM Consortium;
RA  the RIKEN Genome Exploration Research Group Phase I & II Team;
RT  Analysis of the mouse transcriptome based on functional annotation of

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RT 60,770 full-length cDNAs." ;  
 RL Nature 420:563-573(2002).  
 [4]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6J; TISSUE=Testis;  
 RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;  
 RA Carninci P., Shibata Y., Hayatsu M., Sugahara Y., Shibata K., Itoh M.,  
 RA Kono H., Okazaki Y., Muramatsu M., Hayashizaki Y.,  
 RT "Normalization and subtraction of cap-trapper-selected cDNAs to  
 RT prepare full-length cDNA libraries for rapid discovery of new genes." ;  
 RL Genome Res. 10:1617-1630(2000).  
 RN  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6J; TISSUE=Testis;  
 RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;  
 RA Shibata K., Itoh M., Aizawa K., Nagao K., Sasaki N., Carninci P.,  
 RA Kono H., Akiyama J., Nishi K., Kiteunai T., Tashiro H., Itoh M.,  
 RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,  
 RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kasliwagi K.,  
 RA Fujisake S., Inoue K., Togawa Y., Izawa M., Ohara B., Watabiki M.,  
 RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsura S., Kawai J.,  
 RA Okazaki Y., Muramatsu M., Inoue Y., Kita A., Hayashizaki Y.,  
 RT "Riken integrated sequence analysis (RISA) system-384-format  
 RT sequencing pipeline with 384 multicapillary sequencer." ;  
 RL Genome Res. 10:1757-1771(2000).  
 RN  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6J; TISSUE=Testis;  
 RA Adachi J., Aizawa K., Akahira S., Akimura T., Arai A., Aono H.,  
 RA Arakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,  
 RA Hanagaki T., Hara A., Hayatsu N., Hiramoto K., Hiraoka T., Hori F.,  
 RA Inotani K., Ishii Y., Itoh M., Izawa M., Kasukawa T., Kato H.,  
 RA Kawai J., Kojima Y., Kono H., Kouda M., Koya S., Kurihara C.,  
 RA Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numazaki R., Ono M.,  
 RA Okazaki Y., Okido T., Owa C., Saito R., Saito R., Sakai C., Sakai K.,  
 RA Sano H., Sasaki D., Shibata K., Shibata Y., Shingawa A., Shiraki T.,  
 RA Sogabe Y., Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T.,  
 RA Tejima Y., Toya T., Yamamura T., Yasunishi A., Yoshida K., Yoshino M.,  
 RA Muramatsu M., Hayashizaki Y.,  
 RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AK006326; BAB24527.1; -.  
 DR MGD; MGI:1194499; Gsg1.  
 DR GO; GO:0016021; C:integral to membrane; TAS.  
 SO SEQUENCE 217 AA, 24215 MW, C9775AC6478AF1B CRC64;  
 Query Match 45.4%; Score 789.5; DB 2; Length 217;  
 Best Local Similarity 72.9%; Pred. No. 1.4e-62;  
 Matches 151; Conservative 15; Mismatches 38; Indels 3; Gaps 2;  
 QY 120 PPAKRLTLMSTGCTQTYIYIGLPISFLITLTDLLTGNPACGLGSAFAVSVTLGILG 179  
 DB 13 PVAK-VFWLSTLGAQTVYIGLQISFLITLTDLLTGNPACGLGSAFAVSVTLGILG 70  
 QY 180 MVAMHMYSGVFOATVNLGPEDMRPHVWNYGAFYMAVLSPTCCMASAVTTFTTTRVLE 239  
 DB 71 MVAMHLYSGVFOATVNLGPEDMRPHVWNYGAFYMAVLSPTCCMASAVTTFTTTRVLE 130  
 QY 240 FKCKHSKSPKKNPCPLPHHQCF-PRRLSSAAPVGLTGYHQYHNPINHSVSGVDYFS 298  
 DB 131 FKCRHSKSPKKNPCPLPHHQCF-PRRLSSAAPVGLTGYHQYHNPINHSVSGVDYFS 150  
 QY 299 ELANKGQGRGASQELKAVASVBEQ 325  
 DB 191 ALDDKEQGGISQELKAVASVBEQ 217

DE Mus musculus 2 days neonate thymus thymic cells cDNA, RIKEN full-  
 DE length enriched library, clone:R43001020 product:germ cell-specific  
 DE gene 1, full insert sequence.  
 GN Name=Gsg1;  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Rodentia; Scurionath; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=NOD; TISSUE=Thymus;  
 RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;  
 RA Carninci P., Hayashizaki Y.,  
 RT "High-efficiency full-length cDNA cloning." ;  
 RL Meth. Enzymol. 303:19-44(1999).  
 RN  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=NOD; TISSUE=Thymus;  
 RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;  
 RA RIKEN PANTOM Consortium;  
 RT "Functional annotation of a full-length mouse cDNA collection." ;  
 RL Nature 409:685-690(2001).  
 RN  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=NOD; TISSUE=Thymus;  
 RA The PANTOM Consortium;  
 RT "The RIKEN Genome Exploration Research Group Phase I & II Team;  
 RT "Analysis of the mouse transcriptome based on functional annotation of  
 RT 60,770 full-length cDNAs." ;  
 RL Nature 420:563-573(2002).  
 RN  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=NOD; TISSUE=Thymus;  
 RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;  
 RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,  
 RA Kono H., Okazaki Y., Muramatsu M., Hayashizaki Y.,  
 RT "Normalization and subtraction of cap-trapper-selected cDNAs to  
 RT prepare full-length cDNA libraries for rapid discovery of new genes." ;  
 RL Genome Res. 10:1617-1630(2000).  
 RN  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=NOD; TISSUE=Thymus;  
 RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;  
 RA Shibata K., Itoh M., Aizawa K., Nagao K., Sasaki N., Carninci P.,  
 RA Kono H., Akiyama J., Nishi K., Kiteunai T., Tashiro H., Itoh M.,  
 RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,  
 RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kasliwagi K.,  
 RA Fujisake S., Inoue K., Togawa Y., Izawa M., Ohara B., Watabiki M.,  
 RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsura S., Kawai J.,  
 RA Okazaki Y., Muramatsu M., Inoue Y., Kita A., Hayashizaki Y.,  
 RT "Riken integrated sequence analysis (RISA) system-384-format  
 RT sequencing pipeline with 384 multicapillary sequencer." ;  
 RL Genome Res. 10:1757-1771(2000).  
 RN  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=NOD; TISSUE=Thymus;  
 RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,  
 RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hayashizaki Y.,  
 RA Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirazane T.,  
 RA Hori F., Inotani K., Ishii Y., Itoh M., Izawa M., Kasukawa T.,  
 RA Kato H., Kawai J., Kojima Y., Kono H., Kouda M., Koya S.,  
 RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,  
 RA Nishi K., Nomura K., Numazaki R., Ono M., Ohse N., Okazaki Y.,  
 RA Saito R., Saito H., Saito C., Sakai C., Sakai K., Sakazume N., Sano H.,  
 RA Sasaki D., Shibata K., Shingawa A., Shiraki T., Sogabe Y., Tagami M.,  
 RA Tagawa A., Takahashi F., Takahashi A., Takahashi S., Takada Y., Tanaka T.,  
 RA Tomaru A., Toya T., Yasunishi A., Yasunishi M., Hayashizaki Y.,  
 RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AK088285; BAC40258.1; -.  
 DR MGD; MGI:1194499; Gsg1.  
 DR GO; GO:0016021; C:integral to membrane; TAS.  
 SO SEQUENCE 217 AA, 24197 MW, CD371DB7B7156F1B CRC64;



RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blackley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Buttefield Y.S.,  
 RA Kravinsky M.I., Skalska U., Smalim D.E., Schermer A., Schein J.E.,  
 RA Jones S.J., Marra M.A.,  
 RA "Generation and initial analysis of more than 15,000 full-length human  
 RT and mouse cDNA sequences";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

RP SEQUENCE FROM N.A.

RC TISSUE=Eye;

RA Strausberg R.;

RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.

DR EMBL: BC001796; AA001796.1; - F0F7D123255A2935 CRC64;

SO SEQUENCE 282 AA; 31102 MW; 160F7D123255A2935 CRC64;

Query Match 37.0%; Score 643.5; DB 2; Length 282;

Best Local Similarity 51.1%; Pred. No. 2.5e-49;

Matches 162; Conservative 14; Mismatches 76; Indels 65; Gaps 11;

DB 4 MELSKAPSGORTLLSAILSMLSLSPSTTLLSNVYVGTOKYKPKLCEKGLAKCPDMPV 63

DB 1 MELSKAPSGORTLLSAILSMLSLSPSTTLLSNVYVGTOKYKPKLCEKGLAKCPDMPV 60

QY SLDPDNTSTQEVVQYNNMETGDRSPFRSGMWLSCEETVBPGERCSPIELTPPAK 123

DB SLDPDNTSTQEVVQYNNMETGDRSPFRSGMWLSCEETVBPGERCSPIELTPPAK 120

QY 124 REILWLSLGTQITTYIGLOFISFLLLTDLTLGNPAAGLTAFAVSVLSGLG---M 180

DB 121 RGEKGL-----LEFATLQGPCHPTLRFG---GKILMEKASLPSPPLGCGNPM 166

QY 181 VA-----HMYVQVQ---ATVNLGPEWDRPHVNTGMAFYAMLSCTCMASAVTTTNT 232

DB 167 VLPGNADHLHRTSIHQLPPTATNLATN-WEPCLM-----AQTERLCCC----- 208

QY 233 YTRMVLFPKCKSKSKPKENPN-----CLPHNQCPRRLSAA-----PTVGPITSYHQ-- 281

DB 209 -----FLCPVRSRPGDGPDPVFTSLPSPDQLGSRRLTCLMLGILHGLALLHLH 261

QY 282 ----YHNPRIHSVSEGV 294

DB 262 GVGCHLQHVHODGAGV 278

RESULT 12

Q96LP9 PRELIMINARY; PRT; 326 AA.

AC 096LP9; DT 01-DEC-2001 (T-EMBLrel. 19, Created)

DT 01-DEC-2001 (T-EMBLrel. 19, Last sequence update)

DT 01-OCT-2002 (T-EMBLrel. 22, Last annotation update)

DE Hypothetical protein FLJ25316.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

NCBI\_TaxID=9606;

RP SEQUENCE FROM N.A.

RC TISSUE=Testis;

RA Ishihashi T., Kanohori K., Yosida M., Watanabe S., Ishida S., Ono Y.,

RA Houtura T., Hirooka S., Murakawa K., Takiguchi S., Kusano J.,

RA Watanabe M., Fujimori K., Tanai H., Ishida M., Yamashita H., Chiba Y.,

RA Suzuki Y., Hata H., Nakagawa K., Mizuno S., Morinaga M., Kawamura M.,

RA Sugiyama T., Irie R., Otsuki T., Sato H., Nishikawa T., Sugiyama A.,

RA Kawakami B., Nagai K., Isega T., Sugano S.;

RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.

DR EMBL: AK058045; BAB71638.1; - AE22B4CA24971CD CRC64;

SO SEQUENCE 326 AA; 36004 MW; AE22B4CA24971CD CRC64;

Query Match 35.8%; Score 623; DB 2; Length 326;

Best Local Similarity 47.5%; Pred. No. 2e-47;

Matches 162; Conservative 15; Mismatches 76; Indels 88; Gaps 12;

QY 3 XNELSKAPSGORTLLSAILSMLSLSPSTTLLSNVYVGTOKYKPKLCEKGLAKCPDMPV 62

DB 16 MELSKAPSGORTLLSAILSMLSLSPSTTLLSNVYVGTOKYKPKLCEKGLAKCPDMPV 75

QY VSLDGTNTSTQEVVQYNNMETGDRSPFRSGMWLSCEETVBPGERCSPIELTPPAK 108

DB VSLDGTNTSTQEVVQYNNMETGDRSPFRSGMWLSCEETVBPGERCSPIELTPPAK 135

QY 109 -----GERCSPIELTPPAKREILWLSLGTQITTYIGLOFISFLLLTDLTLGNPA 159

DB 136 RSSGTAAGRCRSPFIETLPKRGKGL-----LEFATLQGPCHPTLRFG--- 182

QY 160 CGKLKSAFAVSVLSGLG---MVA-----HMYVQVQ---ATVNLGPEWDRPHVNT 208

DB 183 -GRILMEKASLPSPPLGCGNPMVLPGNADHLHRTSIHQLPPTATNLATN-WEPCLM-- 238

QY 209 GMAFYAMLSFTCCMASAVTTTNTYTRMVLFPKCKSKSKPKENPN-----CLPHNQCPR 264

DB 239 -----AQTERLCCC-----FLCPVRSRPGDGPDPVFTSLPSPDQLGSR 276

QY 265 RLSSAA-----PTVGPITSYHQ-----YHNPRIHSVSEGV 294

DB 277 RLFTCLRLMLGILHGLALLHLHGVCHLQHVHODGAGV 317

RESULT 13

Q6UX04 PRELIMINARY; PRT; 280 AA.

AC 06UX04; DT 05-JUL-2004 (T-EMBLrel. 27, Created)

DT 05-JUL-2004 (T-EMBLrel. 27, Last sequence update)

DT 05-JUL-2004 (T-EMBLrel. 27, Last annotation update)

DE RTRSR831.

OS ORFNames=UNQ5831;

OC Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

NCBI\_TaxID=9606;

RP SEQUENCE FROM N.A.

RX MEDLINE=22887296; PubMed=12975309; DOI=10.1101/gr.1293003;

RA Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D., Brueh J.,

RA Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,

RA Batton D., Foster J., Grimaldi C., Gu Q., Hase P.E., Heldens S.,

RA Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,

RA Lewis L., Liao D., Mark M., Robble E., Sanchez C., Schoenfeld J.,

RA Seshagiri S., Simons L., Singh J., Smith V., Stinson J., Vagstad A.,

RA Vandlen R., Watanabe C., Wleand D., Woods K., Xie M.H., Yamaura D.,

RA Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Zeng D., Wood W.I.,

RA Godowski P.;

RT "The secreted protein discovery initiative (SPDI), a large-scale

RT effort to identify novel human secreted and transmembrane proteins: a

RT bioinformatics assessment.";

RL Genome Res. 13:2285-2270(2003).

DR EMBL: AY358206; AA088573.1; - OFEP923418CB3831 CRC64;

SO SEQUENCE 280 AA; 31250 MW; OFEP923418CB3831 CRC64;

Query Match 30.6%; Score 531; DB 2; Length 280;

Best Local Similarity 35.4%; Pred. No. 3.1e-39;

Matches 111; Conservative 37; Mismatches 56; Indels 110; Gaps 5;

QY 14 RLLSLSLSLSTSTSLSNVYVGTOKYKPKLCEKGLAKCPDMPVSLDGTNTST 73

DB 8 RALLAVALLALTLPATFTLTHWCOGTQVPRKCGCGGAGNC---PNSGANTANST 64

QY 74 QEVVQ-----YNNETGDRSPFRSGMWLSCEETVBPGERCSPI 116

DB 65 AAPAAAAAATASGNGPPGAGLYSWETGDRFLFNPHVGTWYSCBBLISGLGCKRSP 124

QY 117 ELTPPAKREILWLSLGTQITTYIGLOFISFLLLTDLTLGNPAAGLTAFAVSVLSG 176

DB 125 DLAPASR-----G 133

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QY 177 LIGVAVAHMYSOVFOATVNLGPEDMRPHVWNTGMYAFYAMLSFTCCMASAVTTFNTYTM 236
DB 134 LIGVAVAHMYTVOFVTVSLGPEDMRPHSWDGMSCFLAMGSPCCMAASVTTLNSYTK 193
QY 237 VLEPKCKH---SKSPKENDPNCU-----PH 257
DB 194 VLEPRKRKRVFEGYREBEPTFIDPEAIKVFREMERKRDSEEDPHLDCHERYPARHQPH 253
QY 258 HHQCFPRRLSSAP 271
DB 254 MADSWPRSSAOEAP 267

RESULT 14
QY 0726F8 PRELIMINARY; PRT; 194 AA.
AC 0726F8;
DT 01-OCT-2003 (Tremblrel. 25, Created)
DT 01-OCT-2003 (Tremblrel. 25, Last sequence update)
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
DE MGCI18079.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_Taxid=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Li H., Li S., Zhou G., Shen C., Li M., Xiao W., Lin L., Yang S.;
RA Submitted (May-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY302134; AAP57626.1; -.
SQ SEQUENCE 194 AA; 22738 MW; 3B0AB145D1FAB663 CRC64;

Query Match 21.1%; Score 366; DB 2; Length 194;
Best Local Similarity 44.6%; Pred. No. 1.3e-24;
Matches 83; Conservative 30; Mismatches 61; Indels 12; Gaps 6;

QY 151 DLLTGNPACGKLSAPAAVSVLSGLGMVAVAHMYSOVFOATVNLGPEDMRPHVWNTG 210
DB 4 ELFHSSNVTDGKLNFAVFTVLSGLGMVAVAHMYTVOFVTVSLGPEDMRPHSWDGM 63
QY 211 AFYMAWLSFTCCMASAVTTFNTYTMVLEPKCKH---SKSPKENDPNCU---PHHQCFPRRL 266
DB 64 SFCLAMGSPCCMAASVTTLNSYTKVLEPRKRKRVFEGYREBEPTFIDPEAIKYRERM 123
QY 267 SSAAPVPGPLTSTHQVHNQPHISVSGVPIYSRLKRGQKASQGLKKA-VRSSVE-- 323
DB 124 QIEAQR-GRATCPRSHWMEKDGSE-EDFHLDCRERYPARHQPHMADSWPRSSAOEAP 181
QY 324 ---BOC 326
DB 182 ELNRQC 187

RESULT 15
QY 08TB81 PRELIMINARY; PRT; 176 AA.
AC 08TB81;
DT 01-JUN-2002 (Tremblrel. 21, Created)
DT 01-JUN-2002 (Tremblrel. 21, Last sequence update)
DT 01-OCT-2002 (Tremblrel. 22, Last annotation update)
DE Hypothetical protein MGCI18079.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_Taxid=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.L., Feilgold B.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,

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RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Schetz T.E.,
RA Brownstein M.J., Uedon T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Greenwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smalusz D.E., Scherch A., Schein J.B.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RA Strausberg R.;
RA Submitted (Oct-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC016460; AAH16460.1; -.
KW Hypothetical protein.
SQ SEQUENCE 176 AA; 20586 MW; 408A16130B3F252C CRC64;

Query Match 21.0%; Score 365.5; DB 2; Length 176;
Best Local Similarity 45.0%; Pred. No. 1.3e-24;
Matches 72; Conservative 21; Mismatches 28; Indels 39; Gaps 2;

QY 151 DLLTGNPACGKLSAPAAVSVLSGLGMVAVAHMYSOVFOATVNLGPEDMRPHVWNTG 210
DB 4 ELFHSSNVTDGKLNFAVFTVLSGLGMVAVAHMYTVOFVTVSLGPEDMRPHSWDGM 63
QY 211 AFYMAWLSFTCCMASAVTTFNTYTMVLEPKCKH---SKSPKENDPNCU----- 255
DB 64 SFCLAMGSPCCMAASVTTLNSYTKVLEPRKRKRVFEGYREBEPTFIDPEAIKYRERM 123
QY 256 -----PHHQCFPRRLSSAP 271
DB 124 EKRDSEEDPHLDCHERYPARHQPHMADSWPRSSAOEAP 163

Search completed: July 14, 2005, 20:32:20
Job time : 109.168 secs

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